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2272
parameters:
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first 45 summaries

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and is derived by analysis of the total score distribution.
SUMMARIES
description

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Page 1

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	NOVEL GROWTH OR DIFFERENTIATION FACTOR OF THE TGF- beta FAMILY					
	PATENT: WO 9601316-A 1 18-JAN-1996;					
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Page 2

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Tue Oct 15 13:49:36 2002

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 ORGANISM
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 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCES
 1 (bases 1 to 2272) H. sapiens mRNA for actinin beta-C chain.
 2 (bases 1 to 2272) Hoellen G. Res. Commun. 206 (2), 608-613 (1995)
 JOURNAL
 Direct Submission
 Submitted (07-NOV-1994) G. Hoellen, Biopharm GmbH, Czernyting 22,
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ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 2272)
JOURNAL Monomeric protein of the tgf-beta family
PATENT: EP 1074620-A 3 07-FEB-2001;
Hygiene AG (CH)
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BASE COUNT 510 a 663 c 511 g 585 t 3 others
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2269; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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LOCUS AX137805
DEFINITION Sequence 3 from Patent EP1074620.
ACCESSION AX137805
VERSION AX137805.1 GI:14273976
KEYWORDS
SOURCE human.

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 AC063917.20 GI:18449532
 ACCESSION
 VERSION
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 HTG; HTGS_PHASE1; HTGS_DRAFT.
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 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0564P05
----- Summary Statistics -----
Sequencing vector: M13; 87%
Sequencing vector: plasmid: 13%
Chemistry: Dye-primed ET; 87% of reads
Chemistry: Dye-terminator Big Dye; 13% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 172728 bases at least Q40
Consensus quality: 176882 bases at least Q30
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Insert size: 18288; sum-of-contigs
Quality coverage: 3.63 in Q20 bases; agarose-fp
Quality coverage: 4.26 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
consists of 29 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

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Db 184911  ATGGTAGTAGAGCCCTGAGGGGAGGATTTGCTATGTGGTATGAGGAGCCCAAGGTG  184852
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Db 184851  CATGGAAAAACAGCGCCCTACAGAGTGCATCTCTTGAAGAGAGGAGATGACTCATTC  184792
QY  1277  TCTGTCCAGATGTGAGACTCCCTCTTCTGACACATCTTATGAAATTAACCCACCTTTGA  1336
Db 184791  TCTGTCCAGATGTGAGACTCCCTCTTCTGACACATCTTATGAAATTAACCCACCTTTGA  184732
QY  1337  CTTGAAGAAACCTGCATCTAAAGCAAGTCACTGGGCACTCTCGACACTACCTTCTT  1396
Db 184731  CTTGAAGAAACCTGCATCTAAAGCAAGTCACTGGGCACTCTTCTGACACTACCTTCTT  184672
QY  1397  TCTTAGGCGCATAGTCCATCCGCTAGTCCATCCGCTAGCCCTCAGAGGACTCAGAC  1456
Db 184671  TCTTAGGCGCATAGTCCATCCGCTAGTCCATCCGCTAGCCCTCAGAGGACTCAGAC  184612
QY  1457  CCATCTCCACATGACATGACATGCTGCTTCCAGGCAAGAACACCTTATGCTACCT  1516
Db 184611  CCATCTCCACATGACATGACATGCTGCTTCCAGGCAAGAACACCTTATGCTACCT  184553
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QY  1637  TGGATTACACAAAGTTTATGATCACTGTGCCCCAATAATAGAGGCTTACCTACCCCTCTT  1696
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Db 184372  TGTGTGAGCCGCTGCTCTCTTCTTATGTGCGAGTGAACCTACTAAGCTCTTGTGCA  184313
QY  1757  CCTGATCCATTTTGTGCTTCTGCTCTCTGCTTCTATGCTCTTAAGGGGTGACTTGGCT  1816
Db 184312  CCTGATCCATTTTGTGCTTCTGCTCTCTGCTTCTATGCTCTTAAGGGGTGACTTGGCT  184253
QY  1817  GAGCTCTATACCTGAGCTCCCTGCTGCTGCTGCTGCTGCTGAGAGTACGGGATTTCTT  1876
Db 184252  GAGCTCTATACCTGAGCTCCCTGCTGCTGCTGCTGCTGCTGAGAGTACGGGATTTCTT  184193
QY  1877  ATCCCGTTCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  1936
Db 184192  ATCCCGTTCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  184133
QY  1937  CCTACACTACCTGAGCTACCCCTTCCATGAGGCCCAAGCTCTGCTCATTTGATTTT  1996
Db 184132  CCTACACTACCTGAGCTACCCCTTCCATGAGGCCCAAGCTCTGCTCATTTGATTTT  184073
QY  1997  TTTT 2000
Db 184072  GCTT 184069

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RESULT 11
MMU95962 1624 bp mRNA linear ROD 08-MAY-1997
LOCUS Mus musculus actlvin beta c subunit mRNA, complete cds.
DEFINITION

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ACCESSION U95962
 VERSION U95962.1 GI:2072995
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Mus musculus
 REFERENCE 1 (bases 1 to 1624)
 AUTHORS Pang, J., Wang, S.-Q., Smiley, E. and Bonadio, J.
 TITLE Genes coding for mouse activin beta C and beta E are closely linked and exhibit a liver-specific expression pattern in adult tissues
 JOURNAL Blochem. Biophys. Res. Commun. 231 (3), 655-661 (1997)
 MEDLINE 9724404
 REFERENCE 2 (bases 1 to 1624)
 AUTHORS Pang, J., Wang, S.-Q., Smiley, E. and Bonadio, J.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAR-1997) Pathology, University of Michigan Medical School, 1198 SE 300 North Ingalls Building, Ann Arbor, MI 48109-0417, USA
 FEATURES
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 1..1624
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 149..1207
 /note="growth factor"
 /product="activin beta C subunit"
 /protein_id="AAC53164.1"
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 translation="MASSLLALLLEPTVYNPKTEGPCMCAWIAFDLESORELL
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 PVAAGYRVGGRHVRBRGIDOGASRMCCROFDFPEIDIMNITIDPEYAMFC
 TGCPPLVAGMPEISAFHTAVNLKANAAGTTGSGCCVPTSRRLSLTYDRDS
 NIVTDIPDMVYAGCS"
 BASE COUNT 357 a 478 c 415 g 374 t
 ORIGIN
 Query Match 35.4% Score 803.2; DB 10; Length 1624;
 Best Local Similarity 72.8%; Pred. No. 5.6e-207;
 Matches 1151; Conservative 0; Mismatches 383; Indels 48; Gaps 7.1

Db 465 ACCTTCAGCATCAACAGACCCGGCTGAGTTCACCTT---CTCTGTAGATAGGCCA 521
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 Db 522 GTGGCAGTGAAGGTCCGCGACAGCCCGCTCATGTTCTTCTGTGAGTCCCGCAACATGCCA 581
 Oy 561 CTTGAGCTTTGAAGAAGAGATGCTGTGCTGGTGCACATTAATACAACTCACCTTTGG 620
 Db 582 CCCAGACCATGAATATATAGATGTTCTTGCTTAAGACATATACACACCAACCTCACCTTGA 641
 Oy 621 CTATCAGTACCTGCTGAGAGTGTGATGCCAGTGGCTGCGATCACTCCCTAGGCGCTG 680
 Db 642 CAAGTACGATACGGTGGCAGATGCAAGTGGCTGATACAGCTTCTCTGCGGACCTG 701
 Oy 681 AACCTAACCTGCTGACAGCCAGGGGCGACCTGACCTGAGCTGAGCTTGAAGGCCACGG 740
 Db 702 AACCTAACCTGCTGACAGCCAGGGGCGACCTGACCTGAGCTGAGCTTGAAGGCCACGG 761
 Oy 741 TAGCCAGAGCTCAGTCAATCTGGGTGAGAGTCCCATATAGGCTTTTGTGCGACGCCGGG 800
 Db 762 TGSCCCACAGTTCCTTGATCTGGGCTGGTCTTCCACAGGCTTTTGTGCGACGCCAGG 821
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 Oy 861 GATATGCTGTGACAGAGCTTTTGTGACCTCCGTGAGATGAGTGGGAGGAGCTGGA 920
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 Db 1331 AGGGGATCCACCTCTTAAGAGAGTCACT-----AGTGACCAACACCTTCTTCTTCT 1384
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 Db 1385 GGGACATGTTGAGCC-----AGTACACCATCTCTCAAGCTTAAAGTAAATTCAGC 1440
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OY 1221 G 1221
Db 1225 G 1225

RESULT 13

LOCUS A48432 1558 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 3 from Patent WO9601316.
ACCESSION A48432
VERSION A48432.1 GI:2302222
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1558)
AUTHORS Hoellen, G., Neidhardt, H., Bechtold, R. and Pohl, J.
JOURNAL NOVEL GROWTH OR DIFFERENTIATION FACTOR OF THE TGF- beta FAMILY
Patent: WO 9601316-A 3 18-JAN-1996;
BIOPHARM GES ZUR BIOTECHNOLOGI (DE)
Other publication AU 2979895 960125
Other publication DE 19511243 960104.

FEATURES
Location/Qualifiers
1..1558

BASE COUNT 340 a 453 c 398 g 367 t
ORIGIN /organism="Mus musculus"
/db_xref="taxon:10090"

Query Match 34.4% Score 781: DB 6: Length 1558:
Best Local Similarity 79.9% Pred. No. 6.1e-201:
Matches 959: Conservative 0: Mismatches 235: Indels 7: Gaps 3:

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Db 87 CTGATATTAAGCGTTTGGCTCTTAAGAGGCGCTTCCCGACCAATGACCTCTGATTC 146
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OY 441 GCGTGTCCAGCATCAACAGACTGCTTGAATTTGATTTGATTTGATTTGATTTGATTTGATTTG 500
Db 447 ACCTGTCCAGCATCAACAGACCGGCGCTGCAGTTCACATT---CTGTGTGATGATTTGAGCCA 503
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Db 504 GTGAGAGGAGGTCCAGAGCGCAGTCTCATGTTCTTGTGACAGCTCCCTTCAATACCA 563
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OY 1221 G 1221
Db 1224 G 1224

RESULT 14
LOCUS AR038926 1558 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5807713.
ACCESSION AR038926
VERSION AR038926.1 GI:5958289
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1558)
AUTHORS Hoellen, G., Neidhardt, H., Bechtold, R. and Pohl, J.
JOURNAL DNA encoding growth/differentiation factor
Patent: US 5807713-A 3 15-SEP-1998;
FEATURES Location/Qualifiers
1..1558

BASE COUNT 340 a 453 c 398 g 367 t
ORIGIN /organism="unknown"

Query Match 34.4% Score 781: DB 6: Length 1558:
Best Local Similarity 79.9% Pred. No. 6.1e-201:
Matches 959: Conservative 0: Mismatches 235: Indels 7: Gaps 3:
OY 24 CACACTTCTTCAGAGGCGCTTGCAGACAGAGTGGAGACACACCTCTTGAGACC 83
Db 28 CACATCTCTCCAGAGGCGCTTGCAGACAGAGTGGAGACAGAGTGGAGACAG 86

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Oy 1221 G 1221
Db 1224 G 1224

RESULT 15
ARI23395
LOCUS ARI23395 1558 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 3 from patent US 6171584.
ACCESSION ARI23395
VERSION ARI23395.1 GI:14108756
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1558)
AUTHORS Hotten,G., Neidhardt,H., Bechthold,R., Pohl,J. and Paulista,M.
TITLE TGF-beta family
JOURNAL Patent: US 6171584-A 3 09-JAN-2001;
FEATURES
source location/Qualifiers
BASE COUNT 340 a 453 c 398 g 367 t
ORIGIN

Query Match 34.4%; Score 781; DB 6; Length 1558;
Best Local Similarity 79.9%; Pred. No. 6.1e-201;
Matches 959; Conservative 0; Mismatches 235; Indels 7; Gaps 3;

Oy 24 CACACTTCTTCCAGGGGCTGTGGAGCCAGAGAGAGTGTGAGACCAAGCTGTGAGACC 83
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Oy 144 TTCTGGCTTTCTCTCTCTGCTCCCAACGATGGGCTGACAGCTGAGGCTGAGT 203
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Oy 204 GTCCAGCATGTGGGGGCCCACTTGAATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 263
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Db 327 CAGTGTCCAGAGGGGCTTCAAGAGCGGCTGACGCGCTCCGGGGCTGAGCGGAAA 386
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Oy 384 CACTTCTAGAG--GACAAAGAGGAGAGCAAGATGAAATATCACTTGTGAGACAG 440
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Oy 441 GCCTTCCACCATCAACGAGACTGCTTGTATTTTCACTTCTCTGATGAACTGCTG 500
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Oy 561 CTTGACCTTGAAGGTGAGAGTCTTGTGCTGGGTCCACATTAATCAACACTGACCTTGG 620
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Db 564 CCGAGACCATGAAATATAGAGTCTTGTGTGAAGCATATGAGACCAACCTGACCTTGA 623
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GenCore version 5.1.3
Time 256.267 Seconds
Alignments 778 Million cell updates
Copyright (c) 1993
Using sw mod 16
ACTATGATCATCTTCTT 2

3472872

1008
 45 summaries
 Match
 First

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Searched:      flrat_45 summary
               aseqn_03k802.*
               /SIDSI/gcgdata/geneseq/geneseqn-embI/NA1981.DAT.*
               /SIDSI/gcgdata/geneseq/geneseqn-embI/NA1982.DAT.*
               /SIDSI/gcgdata/geneseq/geneseqn-embI/NA1983.DAT.*
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Total:         6

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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score distribution.
and is derived by analysis of summaries

Description-----

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SUMMARIES

Descriptor

----- Description -----
Transforming growth factor- β (TGF- β)
Human TGF- β activator
Murine liver activator
Sequence of mouse TGF- β
Human polynucleotide
Human TGF- β -like clone
TGF- β polynucleotide
Human polynucleotide
Human gene signal

10	194.2	8.5	5314	21	AA658824
11	194.2	8.5	5314	21	AA655540
12	172.8	7.6	8899	23	AA177574
13	172.8	6.8	8825	20	AAV38238
14	153.53	6.7	2125	19	AAV08037
15	142.4	6.3	687	12	AAK94607
16	140.2	6.2	1616	12	AAV16883
17	140.2	6.7	2819	17	AAV38240
18	138.6	6.5	1760	11	AAV70318
19	125.6	5.2	1966	8	AAV70318
20	118.8	5.1	1530	8	AAV70317
21	118	5.2	3588	7	AAV604230
22	116.2	4.8	958	22	AAH56008
23	108.4	4.8	1520	22	AAH56491
24	108.4	4.8	1475	22	AAU0429
25	108.4	4.8	14425	22	AAV001648
26	108.4	4.7	1873	11	AAV70315
27	107.2	4.7	1630	22	AAV08456
28	107.2	4.6	391	22	AA1588656
29	101	4.4	1505	12	AAV08840
30	83.4	3.7	1667	12	AAV08839
31	78.6	3.2	1387	13	AAV38238
32	72.6	3.2	1387	13	AAV02688
33	72.6	3.2	2711	16	AAV06285
34	72.6	3.2	920	18	AAV70316
35	71.6	3.2	926	18	AAV03016
36	71.6	3.2	926	16	AAV03016
37	71.6	3.2	1245	12	AAV03016
38	71.6	3.2	1345	18	AAV03016
39	71.6	3.2	1345	18	AAV03016
40	71.6	3.2	1585	18	AAV03016
41	69.8	3.1	3585	18	AAV03016
42	69.8	3.1	3585	18	AAV03016
43	69.8	3.1	3585	18	AAV03016
44	69.2	3.0	1233	23	AAV03016
45				16	AAV03016

ALIGNMENTS

mouse CLASP-1 nuc1
DNA encoding novel
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human gene express
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Human liver activl
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DNA encoding novel
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XX	RESULT 1
XX	AAT11104
ID	AAT11104 standard; CDNA; 2272 BP.
XX	
XX	AAT11104;
XX	09-AUG-1996 (first entry)
XX	Transforming growth factor beta MP-121 CDNA.
DE	Induction; Promotion; dental implantation
XX	TGF-beta: MP-121; mitogen; differentiation;
KM	maintenance; morphogen; tissue regeneration;
KW	wound healing; ss.
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OS	Homo sapiens.
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XX	location/Qualifiers
FH	128..1186
FT	/tag= a TGF-beta-MP-121
FT	/product=
FT	836..1183
FT	/tag= b
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FT	mat_peptide
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XX	DE19511243-Al.
PN	
XX	04-JAN-1996.
PD	
XX	95DE-1011243.
XX	27-MAR-1995;
FE	14AD-1423190.
XX	01-JUL-1994;
PK	
XX	BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
PA	(BIOP-) BIOPHARM

[illegible]

CC sections within the TGF- β 1 using total RNA from human liver was
CC subcloned and sequenced using primers corresp. to
CC to contain a new sequence, one clone (designated pSK-M121) was
CC used to re-sequence the human liver cDNA library from this clone was
CC found. The present sequence (protein coding for this clone) was
CC identified. The present sequence (protein coding for this clone) was
CC complementary to the TGF- β 1 and a 2272 bp fragment
CC motif (protein) useful for inducing the protein it (so has mitogenic and
CC Sequence 2272 bp; 510 A; 663 C; 513 G; 586 T; 0 other).
Query Match
Best Local Similarity 99.9%; Score 100.0; Expect 0.0
Matches 2272

Best Local Similarity: 99.98%
Matches: 2271 G; 586 T; 0 Other

||||| mismatches
1: 1
length 2272

61 TTGAGACCTCTGTTGAGACCCCTGAGCCGCTGTTCCAGGCGCTTCTGCGACGCCCTGCGAGGACGACGAG 60

121 CCACGCAATGAGCTTCTGGCCCTTTTCAGAGCCTTC 1

[illegible]

dyGGGAG 240
 ..CTTGATCTGCCAAGAACA-
 4 27CTCGCTTGTGGACTGGAC-
 db

481 C⁺.....GACCGCCCTGTGTCAGAGCTTCTTCTTGGACAC 300
 CATCAC.....GACCGCCCTGTGTCAGAGCTTCTTCTTGGACAC 300
 Db

541 GCACCTTGTGAGGACTGCACCTGCAGCA 360

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Abstract—The purpose of this study was to determine the effect of a 10-week training program on the physical fitness of 10-year-old children. The study was conducted in a primary school in the city of Ankara, Turkey. The study group consisted of 20 children (10 boys and 10 girls) who were randomly selected from the 10-year-old children in the school. The children were divided into two groups: a control group and an experimental group. The control group did not participate in any physical education program, while the experimental group participated in a 10-week training program. The physical fitness of the children was measured at the beginning and at the end of the 10-week period. The measurements included maximum heart rate, maximum oxygen consumption, maximum power, and maximum speed. The results of the study showed that the experimental group had significantly higher values for all four measurements at the end of the 10-week period compared to the control group. The results suggest that a 10-week training program can improve the physical fitness of 10-year-old children.

105-09-684-383-1.rng

Page 2

db
721 GCTGCTACCTTGGAGGCCAGGTAGCCCGACACTTGA
|||||...|||..-...CIGCTGCAGCCAGGGGCACCTGTA

[illegible]

841 CGACTGCCAAGSACGCTGTGGTCCAGCATTTCCACCAGCAGCGCTTC
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901 GATTGGCTGCACCAcctgagggcm...ccagaggTTTTTGTGTGACTTCCTC

GCAGTGGCCCACTACATCATCTTTTCATAGG ACC
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 PD 20-NOV-1997; 97MO-US20882.
 PE 20-NOV-1996; 96US-0752919.
 PR (UMM) UNIV MICHIGAN.
 PA Bonadio J, Fang J:
 PI WPI: 1998-312408/27.
 DR P-PSDB: AAM60617.
 XX New isolated nucleic acid encoding sub-units of liver activin -
 PT useful for regulating growth and differentiation of cells, e.g. for
 PT treating liver, bone and hematopoietic disorders
 XX Claim 7; Fig 1; 141pp; English.
 PS This cDNA encodes a murine liver activin beta c polypeptide. Sequences
 CC derived from beta c cDNA clone is used for screening and cloning a liver
 CC activin beta c gene. Disorders of cell growth or differentiation (or
 CC susceptibility to them) are diagnosed by measuring liver activin gene
 CC activity or by detecting a mutation in the liver activin gene. Disorders
 CC of haematopoiesis, erythroid differentiation, ovarian follicular
 CC maturation, hormone secretion, neuronal survival, spermatogenesis, bone
 CC formation, insulin secretion or cardiac morphogenesis are some conditions
 CC that can be diagnosed using the liver activin. Cell growth and
 CC differentiation can be stimulated by treatment with an liver activin
 CC compound or agent that upregulated the compound's expression. Antagonists
 CC can be used to treat liver diseases while agonists can be used to
 CC increase growth and regeneration of liver tissue. The liver activin
 CC compound may also induce bone growth (e.g. for treating osteoporosis or
 CC osteomalacia) or haematopoiesis, particularly erythropoiesis, e.g. for
 CC treating hemophilia, cystic fibrosis or menstrual disorders. Antibodies
 CC are useful in immunoassays, to generate anti-idiotypic antibodies (which
 CC bind to liver activin receptors) and to inhibit liver activin. Also,
 CC transgenic animals containing liver activin gene can be used to produce
 CC the liver activin (in correctly processed and modified forms) proteins,
 CC or the transgenic animals, are useful for screening for liver activin
 CC modulators.
 CC
 SO Sequence 1837 BP; 418 A; 531 C; 455 G; 433 T; 0 other:
 Query Match 36.7%; Score 833.8; DB 19; Length 1837;
 Best Local Similarity 72.4%; Pred. No. 2,4e-185;
 Matches 1196; Conservative 0; Mismatches 407; Indels 48; Gaps 7;

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Oy 1521 TAGACCCCATTAACCACTATGCTTCCTTCCTTACATGCTGCCACTCCAGA 1580
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Oy 1581 TGAGTTGACACACCCCTCCCTCCCAATTTTGTGATCTCCAGAGAGCCCTTTGGA 1640
Db 1560 TGAATGCTTACTAGTCTCTCCCTTGAATCTGTGGCTCTCGAAGAACCCCTTATCAGG 1619
Oy 1641 TTCAACCAAGTTTATGATCATCATCGCTGCCCA 1671
Db 1620 GTCACCTGAAGATTATATTGCTGCTTCCANA 1650

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RESULT 4

AAV69286 standard; DNA: 10708 BP.

AAV69286;

02-FEB-1999 (first entry)

Sequence of mouse activin genetic loci.

Liver activin: beta c; beta e; cell differentiation; haematopoiesis;
 erythroid; ovarian follicular maturation; hormone; neuronal survival;
 spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;
 osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunosassay;
 menstrual disorder; transgenic; modulator; ss.

Mus sp.

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/number- 1

/note- "activin beta e exon 2"

10709..10708

/tag- cd

/number- 1

/note- "activin beta e exon 2"

10709..10708

/tag- ce

/number- 1

/note- "activin beta e exon 2"

10709..10708

/tag- cf

/number- 1

/note- "activin beta e exon 2"

10709..10708</

Oy	437	ACAGGGCTCCACATCAATCAACAGACCTGCTTATTTATTTATCTTCCTGATAGAACT	496
Db	1990	ACAGACCTCTCCAGCATCAACCAAGACCCTGGTCCAGTTCCACTT---CTCTGGTAAMAATG	2046
Oy	497	GCATGTCACAGGAGGATCCAGCAGGCCAGTCTCATGTCTTGTGTGCAGCTCCCTTCAAT	556
Db	2047	GCCAGTGGCATGGAGGATCCGGGACCCGCTTCATGTTCCTTCGGCAGTGTCCCCCAAAAT	2106
Oy	557	ACCACCTTGGACCTTGAAGAATGAGATCCCTTGGTGGGTGCACATATATACCAACCTCAC	616
Db	2107	GCCACCCAGACCACTGAATATTAAGACTTCTTGGCTAAGAACCATATGCACCAACCTCAC	2166
Oy	617	TTGGCTACTAGTACCTGCTGGAGGTGGATGCCAGTGGCTGGCATCACTCCCTTAGGG	676
Db	2167	TTTGACAACTAGTACCTGGTGGCAGGTGAATGCCAGTGGCTGTCACAGCTTCTCTGGGA	2226
Oy	677	CCTGAACTCAAGCTGCTCTGCACGCCAGSGGCCACCTGCACCCCTGGAGCTGTATCTTGAAGG	736
Db	2227	CCCTAACCTCAACCTGCTCTGCACGCCAGGAGACCTTACTCTTGGAGCTGTATCAAGAAAGC	2286
Oy	737	CAGGTAGCCCAAGAGCTCAGTCACTCTGGGTGGAGGTGGCCATAGAGCCCTTTTGTGGCAGCC	796
Db	2287	CAGGTGCCCCACACTTCTTGATCTCTGGGCTGTTTTCCACAGGCCCTTTTGTGGCAGCC	2346
Oy	797	CGGGTGAGAGTGGGGGCAAAACCCAGATTCACGACGACGAGCATTCAGCTGCCAAGAGGG	856
Db	2347	CAGGTAAAGGTTGGAGGCAAGCATCGGGTTCGCCCGCAGAGTATCGATTGCGAGGGGGG	2406
Oy	857	TTCCAGAGTGTGCTGTGCACAAAGATTTTTGTGGACTTCGGTGAATTTGGCTGGACAGAC	916
Db	2407	TTCCAGAGTGTGCTGTGCACAAAGATTTTTGTGGACTTCGGTGAATTTGGCTGGAAATGAC	2466
Oy	917	TGGATCATCCAGCCTGAGGGCTACGGCATGAACCTTCTCATATGGGCACTGCCACTACAC	976
Db	2467	TGGATCATCCAGCCTGAGGGCTATGGCATGAACCTTCTCATATGGGCACTGCCACTACAT	2526
Oy	977	ATAGCAGGCATGCTGCTATTTGCTGCTCTCTTTCACACTGCAGTGGCTCAATCTTCTCAAG	1036
Db	2527	GTGGAGGAGCATGCTGTGCATCTGTGCTCTCTTTCACACTGCAGTGGCTCAATCTTCTCAAA	2586
Oy	1037	GCCAAACAGAGTGCAGGACACACTGAGAGGGGGCTCATGCTGTGTACCCACGGGCCGGGc	1096
Db	2587	GCCAAACAGAGTGTGTGGACACACTGGGAGGGGGCTGTGCTGTCTTACATCTCGCCCC	1646
Oy	1097	CCCCGTCTCTGCTCTATATATGACAGGGAGCAGACATTGTATAGACTGACATACCTGAC	1156
Db	2647	CCCTGTCTTGTCTCTACTATATGACAGGAGCAGACATTGTATAGACGAAATATCTGTAC	2706
Oy	1157	ATGGTATGAGAGGGCTGTGGGTGAGTATCTATGTGTGTGATGGAGGCCCAAGGTG	1216
Db	2707	ATGGTGTGTGAGGGCTGTGGGTGTATGTATGCTTATGGTGTATACAGGCTGGCTTAGAGAG	2766
Oy	1217	CATGGGAAAACAGCGCCCTACAGAAATGCACCTTCTTGAAGAGGGAGATGACCTCATTC	1276
Db	2767	AATGG-----CCTTCTTCAGGAAGGGGAAACCTGTTCCTCC	2801
Oy	1277	TCTGTTCAGAAATGTGAGATCCCTTCTCTGAGAGATCTTATGGAATTAACCCACTTTGA	1336
Db	2802	ACTTCTGTCCAAATGTGAACACTTTCCTTAAGCAT-----GACAGCATCCCTCTGTGGA	2855
Oy	1337	CTTGAAGAAACCTTCAATCTTAAGCAAGTCACTGTGCATCTTCTGACCATTAACCTCTTT	1396
Db	2856	CTTCAAGGGGATCCACTTAAGAAGAGTCACT-----AGTGACAAACAGCTTTCCTTC	1456
Oy	1397	TCTTAAAGGATAGTGCATCCCGCTAGTCAATCCCGGTAGCGCCCACTCCAGGAGTCAAGAC	1456
Db	2910	TGCTGGGCAATGTTGATGCC-----AGTACACCCATCTCTAGCCCTTAAGCTAAGGCTTAAT	2965
Oy	1457	CCATCTCCAAACCATGAGCAATGCCATCTGTGTCCACGACCAACCCCTTAGCTCACT	1516
Db	2966	CGACTGCTTACCAAGCAATGTCAATTTTGT---CCTGGCAAAACACACCTTAGCTCTGCC	3024
Oy	1517	TTAATAGACCCATTAACCACTATGCTCTCTGTCTTCTTACTCAATGTGTCCCACTGC	1576

Db	3025	TTAGTCAACGATGATATATCTACCTGTGCTCCCTGAACCCGACAC-CGGAAAGTTCCTATCC	3083
Oy	1577	AGATGAGTTGACACACACCCCTTCCCAATTTTGTGATCTCCAGAGAGGCCCTTCTT	1636
Db	3084	ACGATGATATGCTTGTAGTGTCTCCCTTGAATCTGTGGCTCTCCGAAGAACCCCTTCAT	3143
Oy	1637	TGGATTCACCAAGTTTGTAGATCATGCTGCCCCAA	1671
Db	3144	CAGGCTCAGTGAAGATTATATTTGCTGCTTCCAA	3178
RESULT 5			
XX	AAK52736/c		
ID	AAK52736	standard; cDNA; 1606 BP.	
XX	AAK52736;		
XX	06-NOV-2001	(first entry)	
DE	Human polynucleotide SEQ ID NO 2265.		
XX	Human polynucleotide SEQ ID NO 2265.		
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy;		
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;		
KW	tissue growth factor; immunomodulatory; cancer; leukemia;		
KW	nervous system disorder; arthritis; inflammation; ss.		
XX	Homo sapiens.		
XX	WO200157190-A2.		
XX	09-AUG-2001.		
XX	05-FEB-2001; 2001WO-US04098.		
XX	03-FEB-2000; 2000US-0496914.		
PR	27-APR-2000; 2000US-0506875.		
PR	20-JUN-2000; 2000US-0598075.		
PR	19-JUL-2000; 2000US-0620325.		
PR	01-SEP-2000; 2000US-0654936.		
PR	15-SEP-2000; 2000US-0663561.		
PR	20-OCT-2000; 2000US-0693325.		
XX	30-NOV-2000; 2000US-0728422.		
PA	(HYSE-) HYSEQ INC.		
PI	Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;		
PI	Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;		
PI	Xue AJ, Yang Y, Wejhrman T, Goodrich R;		
XX	WPI: 2001-476283/51.		
DR	P-SDB: AAK79603.		
PT	Nucleic acids encoding polypeptides with cytokine-like activities,		
PT	useful in diagnosis and gene therapy -		
PS	Claim 1: Page 4608; 6221pp: English.		
XX	The invention relates to polynucleotides (AAK51456-AAK53435) and the		
CC	encoded polypeptides (AAK78323-AAK80302) that exhibit activity elating to		
CC	cytokine, cell proliferation or cell differentiation or which may induce		
CC	production of other cytokines in other cell populations. The		
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or		
CC	peptide therapy. The polypeptides have various cytokine-like activities,		
CC	e.g. stem cell growth factor activity, haematopoiesis regulating		
CC	activity, tissue growth factor activity, immunomodulatory activity and		
CC	activity/inhibit activity and may be useful in the diagnosis and/or		
CC	treatment of cancer, leukemia, nervous system disorders, arthritis and		
CC	inflammation.		
CC	Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666		
CC	(AAK80020) are omitted as the relevant pages from the sequence listing		
CC	were missing at the time of publication.		

PR useful in diagnosis and gene therapy -
XX
PS Claim 1; Page 1259-1260; 6221pp; English.
XX
CC The invention relates to polynucleotides (AA51456-AA53435) and the
CC encoded polypeptides (AAW8333-AAW8302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoietic regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAW80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 1783 BP; 511 A; 265 C; 519 G; 488 T; 0 other;
Query Match 11.6%; Score 263.4; DB 22; Length 1783;
Best Local Similarity 99.6%; Pred. No. 9.2e-52;
Matches 264; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2008 TTTTGAAGTAAATTCCTTAATTTTATTCCTGACACACCAATTTTACAG 2067
DB 1602 TATTGAAAGTTAAATTCCTTAATTTTATTCCTGACACCAATTTTACAG 1543
OY 2068 GGCATATATACCTGATGTAATGAAAGAAAGAAAGCAACCTACACAGATTAAG 2127
DB 1542 GGCATATATACCTGATGTAATGAAAGAAAGAAAGCAACCTACACAGATTAAG 1483
OY 2128 ACCTGAGAAATGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 2187
DB 1482 ACCTGAGAAATGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1423
OY 2188 CAAACGTGCTATGACAGCTCTGAAACAAGAGGTTTCTGTTTAAGCTCAGTAACCT 2247
DB 1422 CAAACGTGCTATGACAGCTCTGAAACAAGAGGTTTCTGTTTAAGCTCAGTAACCT 1363
OY 2248 TTCTGACTATGATCATCTCTT 2272
DB 1362 TTCTGACTATGATCATCTCTT 1338
RESULT 8
AA160442/c
ID AA160442 standard; cDNA: 3678 BP.
XX
AC AA160442;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 4431.
XX
XX Human; neotrophic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemokine;
XX chemokine; thrombolytic; drug screening; arthritis; inflammation;
XX leukemia; ss.
XX
OS Homo sapiens.
XX
PN W020015312-A1.
XX
PD 26-JUL-2001.
XX
XX 26-DEC-2000; 2000MO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX
PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QX, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
XX
XX P-PSDB: AAM41286.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -
XX
XX Claim 1; SEQ ID NO 4431; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and
XX the encoded polypeptides (AAW38642-AAW42213) with neotrophic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localized neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: Immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokine activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukemias and
XX C.N.S disorders.
XX Note: The sequence data for this patent did not form part of the printed
XX specification.
SQ Sequence 3678 BP; 1117 A; 550 C; 877 G; 1134 T; 0 other;
Query Match 11.6%; Score 263.4; DB 22; Length 3678;
Best Local Similarity 99.6%; Pred. No. 1.2e-51;
Matches 264; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2008 TTTTGAAGTAAATTCCTTAATTTTATTCCTGACACCAATTTTACAG 2067
DB 1566 TATTGAAAGTTAAATTCCTTAATTTTATTCCTGACACCAATTTTACAG 1507
OY 2068 GGCATATATACCTGATGTAATGAAAGAAAGAAAGCAACCTACACAGATTAAG 2127
DB 1506 GGCATATATACCTGATGTAATGAAAGAAAGAAAGCAACCTACACAGATTAAG 1447
OY 2128 ACCTGAGAAATGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 2187
DB 1446 ACCTGAGAAATGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1387
OY 2188 CAAACGTGCTATGACAGCTCTGAAACAAGAGGTTTCTGTTTAAGCTCAGTAACCT 2247
DB 1386 CAAACGTGCTATGACAGCTCTGAAACAAGAGGTTTCTGTTTAAGCTCAGTAACCT 1327
OY 2248 TTCTGACTATGATCATCTCTT 2272
DB 1326 TTCTGACTATGATCATCTCTT 1302
RESULT 9
AA119615/c
ID AA119615 standard; cDNA to mRNA: 254 BP.
XX
XX AA119615;
XX
XX 28-JUN-1996 (first entry)
XX
XX

DE Human gene signature HUMS00682.

XX Gene signature: messenger RNA; mRNA; relative abundance; frequency;
 KW human; cloning; mapping; non-biased library; diagnosis; detection;
 KW cell typing; abnormal cell function; ss.

OS Homo sapiens.

PN MO9514772-A1.

XX 01-JUN-1995.

PD 11-NOV-1994; 94MO-JP01916.

XX 12-NOV-1993; 93JP-0355504.

XX (MATS/) MATSUBARA K.

PA (OKUBO/) OKUBO K.

PI Matsubara K, Okubo K;

XX WPI; 1995-206931/27.

PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
 PT for diagnosis of abnormal cell function, by preparing cDNA that
 PT reflects relative abundance of corresp. mRNA in specific human
 PT tissues

PS Claim 1; Page 432; 2245pp; Japanese.

XX A single-stranded DNA (or its complementary strand or the corresp.
 CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
 CC given in AAT19001-726837 and which is able to hybridise to part of
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
 CC sequences were obtained from 3'-directed cDNA libraries prepared
 CC from various human tissues; synthesis of cDNA was initiated from the
 CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
 CC untranslated sequence is unique to a particular mRNA species, almost
 CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
 CC is constructed so as to reflect accurately the relative abundance of
 CC different mRNAs in the particular tissue from which it was derived.
 CC The appearance frequency of a given GS in a cDNA library can be
 CC determined (esp. using primers and probes derived from the GS
 CC sequences) as a means of diagnosing abnormal cell function or for
 CC recognising different cell types.

XX Sequence 254 BP; 74 A; 41 C; 46 G; 93 T; 0 other;

Query Match 11.2%; Score 254; DB 16; Length 254;

Best Local Similarity 100.0%; Pred. No. 6.9e-50; Mismatches 0; Indels 0; Gaps 0;

Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2009 TTGAAAAGTTAAATTCCTTAATTTTATTCCTGTCGACACACCAATTTACAGG 2068

DB 254 TTGAAAAGTTAAATTCCTTAATTTTATTCCTGTCGACACACCAATTTACAGG 195

OY 2069 GCAATATACCTGATGTAAGAAAAGAAAAGAAAAGCAAGCTACCAAGATTAAGA 2128

DB 194 GCAATATACCTGATGTAAGAAAAGAAAAGAAAAGCAAGCTACCAAGATTAAGA 135

OY 2129 CCTCAGGAATGTACATCATTAATGACACATTCGATTAAATCAATAGCTGCTTTTGC 2188

DB 134 CCTCAGGAATGTACATCATTAATGACACATTCGATTAAATCAATAGCTGCTTTTGC 75

OY 2189 AAAGTGTGCTATGACAGCTGCAACAGAGGTTTCTGTTAAAGCTGAGTAACCTTT 2248

DB 74 AAAGTGTGCTATGACAGCTGCAACAGAGGTTTCTGTTAAAGCTGAGTAACCTTT 15

OY 2249 TCTGACATGATGC 2262

DB 14 TCTGACATGATGC 1

RESULT 10

AC87968/c

ID AC87968 standard; cDNA; 5214 BP.

AC AC87968;

DT 07-MAR-2001 (first entry)

DE Mouse CLASP-1 nucleotide sequence SEQ ID NO:2.

XX CLASP-1; CLASP-2; transmembrane protein; immune response; inflammatory;
 KW cadherin-like asymmetry protein; autoimmune disease; immunosuppressive;
 KW immunomodulatory; anti-inflammatory; antitumoric; cytostatic;
 KW hypotensive; antineumatic; antineumatic; haemostatic; neuroprotective;
 KW hypersensitivity; transplantation rejection response; immunodeficiency;
 KW proliferation; differentiation; inflammatory response; arthritis;
 KW inflammatory bowel disease; haematopoietic cell; blood protein disorder;
 KW anaemia; thrombocytopenia; multiple sclerosis; rheumatoid arthritis;
 KW endometriosis; pregnancy induced hypertension; ss.

XX Mus musculus.

PN WO200061747-A2.

PD 19-OCT-2000.

PF 13-APR-2000; 2000MO-US10158.

PR 14-APR-1999; 99US-0129171.

PR 14-MAY-1999; 99US-0134114.

PR 14-MAY-1999; 99US-0134117.

PR 21-OCT-1999; 99US-0160860.

PR 29-OCT-1999; 99US-0162498.

PR 13-DEC-1999; 99US-0170453.

PR 14-JAN-2000; 2000US-0176195.

PR 14-FEB-2000; 2000US-0182296.

XX (ARBO-) ARBOR VITA CORP.

XX Lu PS;

DR WPI; 2000-619230/59.

DR P-PSDB; AAB36521.

PT Isolated cadherin-like asymmetry protein-2 polynucleotide and

PT polypeptide used to diagnose, treat and prevent autoimmune diseases and

XX inflammatory responses -

XX Claim 1; Page 271-276; 286pp; English.

XX The present invention describes cadherin-like asymmetry protein-2
 CC (CLASP-2). CLASP-2 can have immunosuppressive, immunomodulatory,
 CC anti-inflammatory, antitumoric, cytostatic, hypotensive, antineumatic,
 CC antineumatic, haemostatic and neuroprotective activities. CLASP-2 can be
 CC used to inhibit an immune response in a subject by interfering with the
 CC ability of a CLASP-2 protein to bind to another T cell or B cell. An
 CC immune response in a subject may also be inhibited by administering an
 CC antibody which specifically binds to CLASP-2. CLASP-2 polynucleotides,
 CC proteins and antibodies can be used to prevent or treat a CLASP-2
 CC mediated disease, such as an autoimmune disease caused or exacerbated
 CC by increased activity of Th1 cells. They can also be used to treat
 CC hypersensitivities, prevent transplantation rejection responses and
 CC augment immune responsiveness in immunodeficiency states. Inhibitory
 CC proliferation and differentiation of cells involved in an inflammatory
 CC response e.g. arthritis, inflammatory bowel disease and increase
 CC differentiation and proliferation of haematopoietic cells e.g. to treat
 CC anaemia, thrombocytopenia and other blood protein disorders. Disorders
 CC treated by disrupting CLASP-2 function include multiple sclerosis,
 CC rheumatoid arthritis, endometriosis and pregnancy induced hypertension.
 CC The present sequence encodes mouse CLASP-1 which is used in the
 CC exemplification of the present invention.

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid coding sequences. AAS64197-AAS94564 represent novel human
CC diastolic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp://wipo.int/pub/published_nptcsequences](http://wipo.int/pub/published_nptcsequences).
XX

Sequence 899 BP; 239 A; 116 C; 285 G; 259 T; 0 other;

Query Match	7.68;	Score 172.4;	DB 23;	Length 899;
Best Local Similarity	93.98;	Pred. No. 1.4e-30;		
Matches 201; Conservative	0;	Mismatches 11;	Indels 2;	Gaps 2

Accession	Sequence	Position
Oy	TTTAAAGGTAAAAATTCCTTAATTTTTTATTCCTGGTACCACTACCAAAATTACAG	2066
Dh	TTTGAAAAGTTAAAAATTCCTTAATTTTTTATTCCTGGTACCACTACCAAAATTACAG	840
Oy	GCATATATACCTGATGATATGAAAAAGAAAAAGACAAAGCTACACAGATATAAGA	2128
Dh	GCATATATACCTGATGATATGAAAAAGAAAAAGACAAAGCTACACAGATATAAGA	780
Oy	CCTAGAGAAATGTACATCTTAATTACACACTACATTGC-ATTATCAATAGCTGCATTTTG	2187
Dh	CCTAGAGAAATGTACATCTTAATTACACACTACATTGCATTAATCAAAATAGTGCACCTTTTG	720
Oy	C-AAACTGTGGCTATGACACTCCTGAACAAGAG 2220	
Dh	CAAACTGTGGCTATGACACTCCTGAACAAG 686	

Result	ID	Standard	CDNA	Size (bp)
RESULT 13	AA217574/c			
XX	AA217574	standard	CDNA	825 BP.
XX				
AC	AA217574			
XX				
DT	12-OCT-1999	(first entry)		
XX				
DE	Human gene expression product	CDNA sequence	SEQ ID NO:5047	

(HYSE-) HYSEQ INC.
PA
XX
XX
PI Crkventjakov R, Dickson M, Drmanac R, Drmanac S;
PI Escobedo J, Garcia PD, Garcia V, Glise K, Imils MA;
PI Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
PI Lammson G, Leshovoltz D, Pot D, Randazzo F, Reinhard C;
PI Stache-Grain B, Studduth-Klinger J, Williams LT;
XX
XX WPI: 1999-494092/41.

	novel human genes and their expression products which are differentially expressed in different cell types
PT	
PI	
XX	

PS Claim 1; page 2400-2401; 2479pp; English.
XX

The present invention describes a library of human polynucleotides comprising the sequences given in AA121532 to AA217779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AA121532 to AA217779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purposes, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for peptide analogues and antagonists.

SQ Sequence 825 BP; 239 A; 120 C; 162 G; 252 T; 52 other;

Query Match	6.88;	Score 153.8;	DB 20;	Length 825;
Best Local Similarity	90.68;	Pred. No. 3.2e-26;		
Matches 231; Conservative	0;	Mismatches 14;	Indels 10;	Gaps 6

QY	2008	TTTTTAAAGTTAAAAATTCCTTA-----TTTTTATTCGTGTACACATTCAC--AAT	206
Db	324	TATTTAAAGTTAAAAATTCCTTAATTTTTTATTTATTCGTGGTACACATCCNCAAT	265
QY	2062	TTACAGGCGCAATATA--CCTGATCTAATGAAAAAGAAAAAGAAAAAGCAAAAGCTA--CAACA	2119
Db	264	TTCCGGGCAATATACCTCATGTATGAAAAAGAAAAAGAAAAAGCAAAAGCTACACACA	205
QY	2120	GATTAACACCT--CAGAAATGTATCATCTTAATGGACATCTACATTCGATTAATCATACGCTG	2178
Db	204	GATTAAGAACCCGACAGAAATGTACATCTAATGTAGACATACATTCGATTAATCATACGCTG	145
QY	2179	CACCTTTTGCAAACTGTGGCTATGACAGTCTGAAACAAGAAAGG--TTTCCTGTGTTAACT	2237
Db	144	CACCTTTTGCAAACTGTGGCTATGACAGTCTGAAACAAGAAAGGCTTTTCTGTGTTAACT	85
QY	2238	GCAGTAACCTTTTCG 2252	
Db	84	GCAGTAACCTTTTCG 70	

RESULT	14
AAV38238	
AAV38238	standard; CDNA: 2125 BP.
AC	
XX	
AAV38238;	
01-FEB-1999	(first entry)
XXA	
Murine liver activin beta e polypeptide encoding cDNA	

KW Liver activin; beta c: beta e: cell differentiation; haematopoiesis;
 KM erythroid; ovarian follicular maturation; hormone; neuronal survival;
 KM spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;
 KM osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunos assay;
 KM menstrual disorder; transgenic; modulator; ss.
 OS Mus sp.
 XX
 XX
 FT Key Location/Qualifiers
 FT CDS 216..1268
 FT /*tag= a
 FT /product= "activin beta e polypeptide"
 FT sig_peptide /product= 216..278
 FT /*tag= b
 FT mal_peptide 279..1265
 FT /*tag= c
 FT
 XX
 XX W09822492-A1.
 XX
 XX PD 28-MAY-1998.
 XX
 XX PE 20-NOV-1997; 97MO-US20882.
 XX PR 20-NOV-1996; 96US-0752919.
 XX (UNMI) UNIV MICHIGAN.
 XX PA
 XX P1 Bonadio J, Fang J;
 XX DR WPI: 1998-312408/27.
 XX DR P-PSDB: AAM0618.
 XX
 PT New isolated nucleic acid encoding sub-units of liver activin -
 PT useful for regulating growth and differentiation of cells, e.g. for
 PT treating liver, bone and haematopoietic disorders
 XX
 XX
 PS Claim 2: Fig 2: 141pp: English.
 XX
 CC This cDNA encodes a murine liver activin beta e polypeptide. Sequences
 CC derived from a beta c cDNA clone is used for screening and cloning the
 CC activin beta e gene. Disorders of cell growth or differentiation (or
 CC susceptibility to them) are diagnosed by measuring liver activin gene
 CC activity or by detecting a mutation in the liver activin gene. Disorders
 CC of haematopoiesis, erythroid differentiation, ovarian follicular
 CC maturation, hormone secretion, neuronal survival, spermatogenesis, bone
 CC formation, insulin secretion or cardiac morphogenesis are some conditions
 CC that can be diagnosed using the liver activin. Cell growth and
 CC differentiation can be stimulated by treatment with an liver activin
 CC compound or agent that upregulates the compound's expression. Antagonists
 CC can be used to treat liver diseases while agonists can be used to
 CC increase growth and regeneration of liver tissue. The liver activin
 CC compound may also induce bone growth (e.g. for treating osteoporosis or
 CC osteomalacia) or haematopoiesis, particularly erythropoiesis, e.g. for
 CC treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies
 CC are useful in immunoassays, to generate anti-idiotypic antibodies (which
 CC bind to liver activin receptors) and to inhibit liver activin. Also,
 CC transgenic animals containing liver activin gene can be used to produce
 CC the liver activin (in correctly processed and modified forms) proteins,
 CC or the transgenic animals, are useful for screening for liver activin
 CC modulators.
 XX
 XX
 SQ Sequence 2125 BP; 481 A; 573 C; 575 G; 496 T; 0 other:
 XX
 Query Match 6 78: Score 153; DB 19; Length 2125;
 Best Local Similarity 67.66; Pred. No. 7e-26; Indels 6; Gaps 1
 Matches 232; Conservative 0; Mismatches 105;
 844 CTGCCAAGAGGGTCCAGGATGCTGCTCCACAAGAGTTTGTGTGAGCTCGTAGAT 903
 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db CTGTGAGGCTGTAGAGCCCTTATGTGTGTAGGCGAGACCACTATGTAGACTTCAGAGACT 991
 904 TGGCTGCGACGACATCTGATCATCCAGGCTGAGGGCTACGCCATGAACTTCTGATAGGGCA 963

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Db      992 GGGGTGCGGGAGTTGGATTCCTGCACGCCGAGGGATTACCAGTGAATTACTGCAGTGGSACA   1051  
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QY     964 GTCCCACTACACATAAGCAGCATGCTGGTAATTCCTGCTCTTTCACACTGCAGTCTCT   1023  
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Db     1052 GTCCCCGCCCCCACACGTGGCTGCACGTCTGGCACATTGCTGCTCTTCATCTGCCTCTT   1111  
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OY    1024 CAATCTTCCAAGGCGAACACAGCTGCAGGACACCATGAGGGGGGCTCATGCTGTGTACC   1083  
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Db    1112 TAGCCTCTCAAAGCCMACMCACCT-----TGCCCTGGCGGGTTCCTGCTGTGTCCC   1165  
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QY    1084 CACGGCCCGGGCCCCCTGCTCTGCTCTCTAATTAAGACAGGAGCAGACATTTGTCAAGAC   1143  
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Db    1166 CACTGCACGAGAAGCCCTCTCTCTCTCTACCTTGACACATAAATGAGCAATGTGTCMAAGC   1225  
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QY    1144 TGCAATACCTGCATGTAGTAGAGAGCCCTGGGGGTGCAGTTAG   1186  
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Db    1226 CGATGTGCCAGACATGTAGTAGAGGCCCTGTGCTGCAGCTAG   1268  
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RESULT 15
AAQ10891
ID AAQ10891 standard; DNA; 687 BP.

XX AAQ10891;
AC
DT 13-MAY-1991 (first entry)
XX
DE Encodes Xenopus Bone Morphogenetic Factor M3.
XX BMF; osteoporosis; fracture; cartilage; ss.
XX
OS Xenopus laevis.
XX
FH Location/Qualifiers
FT Mat_peptide 2..478 /tag= a
FT /product= BMP M3
FT
XN EP416578-A.
PM 13-MAR-1991.
PD
PE 05-SEP-1990; 90EP-0117079.
PP
PR 20-JUL-1990; 90JP-0190774.
PR 06-SEP-1989; 89JP-0229250.
XX
PA (TAKE) TAKEDA CHEMICAL IND KK.
PA (SCIT-) SCITECH RESEARCH CO.
PI Murakami K, Ueno N, Kato Y;
PI WPI; 1991-075112/11.
DR P-PDB; AARI0991.
XX
PT Xenopus laevis bone morphogenetic protein and DNA encoding it -
PT used in therapy of fracture or osteoporosis
PS Claim 5; Fig 2; 28pp; English.
PS
XX A Xenopus laevis liver-derived DNA library in Charon 28 vector, was
CC screened with a rat activin beta-A cDNA probe. Five clones were
CC isolated, including clone M3. They were subcloned in pUC19 and used
CC to transform competent E.coli HB101 cells. Transformant E.coli HB101/
CC phx3 coding for the M3 BMP was sequenced.
CC See also AAQ10890 and AAQ10892-7.
CX
SQ Sequence 687 BP; 210 A; 145 C; 149 G; 179 T; 4 other;

Query Match 6.3%; Score 142.4; DB 12; Length 687;
Best Local Similarity 60.0%; Pred No. 1.4E+23;
Matches 277; Conservative 0; Mismatches 176; Indels 9; Gaps 2;

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2002, 16:51:16 Search time 52.7958 seconds
(Without alignments)
10570.520 Million cell updates/sec

Title: US-09-684-383-1

Perfect score: 2272
Sequence: 1 CAAGGAGCCATGCGACGCTGCTT 2272

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:
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5: /cgn2_6/ptodata/1/lna/PCITUS.COMB.seq.*
6: /cgn2_6/ptodata/1/lna/Backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2272	100.0	2272	1	US-08-482-577B-1
2	2272	100.0	2272	3	US-08-289-222E-2
3	2272	100.0	2272	4	US-09-218-176-1
4	2272	100.0	2272	4	US-09-054-526B-2
5	781	34.4	1558	4	US-08-482-577B-3
6	781	34.4	1558	4	US-09-218-176-3
7	265	11.7	265	4	US-08-289-222E-5
8	265	11.7	265	4	US-09-054-526B-5
9	142.4	6.3	687	1	US-08-455-550-2
10	140.2	6.2	360	2	US-08-274-215A-11
11	140.2	6.2	360	2	US-08-765-662-11
12	140.2	6.2	360	3	US-09-184-933-11
13	140.2	6.2	360	3	PCT-US95-08745-11
14	140.2	6.2	2419	2	US-08-765-662-13
15	140.2	6.2	2419	5	PCT-US95-08745-13
16	125.6	5.5	1966	1	US-08-197-792-44
17	125.6	5.5	1966	1	US-08-459-850-44
18	125.6	5.5	1966	1	US-08-459-850-44
19	119.2	5.2	1524	1	US-08-459-214-34
20	119.2	5.2	1524	1	US-08-459-850-34
21	119.2	5.2	1524	1	US-08-459-214-34
22	118	5.2	3588	1	US-08-197-792-32
23	118	5.2	3588	1	US-08-459-850-32
24	108.4	4.8	1633	1	US-08-459-214-42
25	108.4	4.8	1633	1	US-08-197-792-42
26	108.4	4.8	1633	1	US-08-459-850-42
27	108.4	4.8	1633	1	US-08-459-214-42

28	92.8	4.1	7218	1	US-08-232-463-14	Sequence 14, Appl
29	83.4	3.7	1657	1	US-08-455-550-1	Sequence 1, Appl1
30	71.6	3.2	926	3	US-08-362-670B-1	Sequence 1, Appl1
31	71.6	3.2	926	3	US-08-333-576C-1	Sequence 1, Appl1
32	71.6	3.2	926	5	US-08-808-324-1	Sequence 1, Appl1
33	71.6	3.2	926	5	PCT-US94-14030A-1	Sequence 1, Appl1
34	71.6	3.2	1345	4	US-08-362-670B-33	Sequence 33, Appl
35	71.6	3.2	1345	4	US-08-333-576C-33	Sequence 33, Appl
36	71.6	3.2	1345	4	US-08-808-324-33	Sequence 33, Appl
37	71.6	3.2	1345	5	PCT-US94-14030A-33	Sequence 33, Appl
38	69.8	3.1	3585	3	US-08-362-670B-9	Sequence 9, Appl1
39	69.8	3.1	3585	3	US-08-333-576C-9	Sequence 9, Appl1
40	69.8	3.1	3585	4	US-08-808-324-9	Sequence 9, Appl1
41	69.8	3.1	3585	5	PCT-US94-14030A-9	Sequence 9, Appl1
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43	69.2	3.0	1233	3	US-08-333-576C-27	Sequence 27, Appl
44	69.2	3.0	1233	4	US-08-808-324-27	Sequence 27, Appl
45	69.2	3.0	1233	5	PCT-US94-14030A-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-08-482-577B-1
Sequence 1, Application US/08482577B
Patent No. 5807713
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAI, MARCELSTEIN, MURRAY, AND ORAM
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08482,577B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KIESNER, SHARON
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P564-5010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2272 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-577B-1
Query Match 100.0%; Score 2272; DB 1; Length 2272;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CAGAGAGCCATGCGAGTGGACACACACTTCTCCAGGGCCTGGGACGACAGAG 60
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2101 AAAAGCAAGCTGTCAGCAAGATGAGTGCAGCAAGCTTCTGTCAGCATCTTATGAA 2160
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2161 TGCATTAATCAATGTCAGCAAGATGAGTGCAGCAAGCTTCTGTCAGCATCTTATGAA 2220
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2221 GGTTCCTGTCAGCAAGATGAGTGCAGCAAGCTTCTGTCAGCATCTTATGAA 2272
2221 GGTTCCTGTCAGCAAGATGAGTGCAGCAAGCTTCTGTCAGCATCTTATGAA 2272

RESULT 3
US-09-218-176-1
Sequence 1, Application US/09218176
Patent No. 6171584
GENERAL INFORMATION:
APPLICANT: H. TEN, Gertrud
APPLICANT: NEIDHARDT, Helge
APPLICANT: BECHTOLD, Rolf
APPLICANT: POHL, Jens
APPLICANT: PAULISTA, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
STREET: 655 Fifteenth Street, N. W., G Street Lobby,
STREET: Suite 330
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218,176
FILING DATE: Herewith
CLASSIFICATION:
APPLICATION NUMBER: 08/679,048
FILING DATE: 12-JUL-1996
CLASSIFICATION:
APPLICATION NUMBER: PCT/EP96/03065
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 2-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,577
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92 102 324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 11 243.1
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: KITS, Monica Chiu
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-6010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2272 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-218-176-1
Query Match 100.0%; Score 2272; DB 4; Length 2272;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAAGAGCCATGACAGTGGACACACACTTCTCCAGGGCTCTGGAGCCAGACAG 460
DB 1 CAAGAGCCATGACAGTGGACACACACTTCTCCAGGGCTCTGGAGCCAGACAG 60
OY 61 TTGAGACACAGCTGTGAGACCCCTGAGCTGTATTTCTCAAGAGGCTTTC 120
DB 61 TTGAGACACAGCTGTGAGACCCCTGAGCTGTATTTCTCAAGAGGCTTTC 120
OY 121 CCCAGCAATGACCTTCTATTTCTTGGCTTCTCTCTCTCTCTCAACACAGTGGC 180
DB 121 CCCAGCAATGACCTTCTATTTCTTGGCTTCTCTCTCTCTCTCAACACAGTGGC 180
OY 181 CACTCCCAAGAGTGGCGGTCACTGTCCAGCATGTGGGGGGCCACCTTGGAACTGGAG 240
DB 181 CACTCCCAAGAGTGGCGGTCACTGTCCAGCATGTGGGGGGCCACCTTGGAACTGGAG 240
OY 241 CCAGGGGGAGCTGTCTTGTATCTGGCCAGAGCAATCTTGGACAAAGCTGACCTAC 300
DB 241 CCAGGGGGAGCTGTCTTGTATCTGGCCAGAGCAATCTTGGACAAAGCTGACCTAC 300
OY 301 CCAGGGGGAGCTGTCTTGTATCTGGCCAGAGCAATCTTGGACAAAGCTGACCTAC 360
DB 301 CCAGGGGGAGCTGTCTTGTATCTGGCCAGAGCAATCTTGGACAAAGCTGACCTAC 360
OY 361 CCTCCAGGGGGTCCACAGGGGGCACTTCTAGAGCAACAGAGGAGAACTGTGAAT 420
DB 361 CCTCCAGGGGGTCCACAGGGGGCACTTCTAGAGCAACAGAGGAGAACTGTGAAT 420
OY 421 CATCAGCTTGTGAGACAGGCTCTCCACATCAACAGCAAGACTGCTTGAATTTTCACTT 480
DB 421 CATCAGCTTGTGAGACAGGCTCTCCACATCAACAGCAAGACTGCTTGAATTTTCACTT 480
OY 481 CTCCTGTATAGACACTGTGTGTGACAGGAGAGTCCAGCAGGCACTTCATATTTTGT 540
DB 481 CTCCTGTATAGACACTGTGTGTGACAGGAGAGTCCAGCAGGCACTTCATATTTTGT 540
OY 541 GCAGCTCCCTCCATATACACTTGTGAGAGTGAAGTGAAGTCTTGTGTGTGTGAC 600
DB 541 GCAGCTCCCTCCATATACACTTGTGAGAGTGAAGTGAAGTCTTGTGTGTGTGAC 600
OY 601 TAATACCAACCTGACCTTGTGAGAGTGAAGTGAAGTCTTGTGTGTGTGAC 660
DB 601 TAATACCAACCTGACCTTGTGAGAGTGAAGTGAAGTCTTGTGTGTGTGAC 660
OY 661 TCAACTCCCCCTGAGGCTGAGAGTGAAGTGAAGTCTTGTGTGTGTGAC 720
DB 661 TCAACTCCCCCTGAGGCTGAGAGTGAAGTGAAGTCTTGTGTGTGTGAC 720
OY 721 GCTGTACTTGAAGGCGAGGTAGCCAGAGCTGATCTGTGGTGTGAGCTGCCATAG 780
DB 721 GCTGTACTTGAAGGCGAGGTAGCCAGAGCTGATCTGTGGTGTGAGCTGCCATAG 780
OY 781 GCTGTACTTGAAGGCGAGGTAGCCAGAGCTGATCTGTGGTGTGAGCTGCCATAG 840
DB 781 GCTGTACTTGAAGGCGAGGTAGCCAGAGCTGATCTGTGGTGTGAGCTGCCATAG 840
OY 841 CGATGGCAAGAGGCTGAGAGTGTCTGTGACAAAGTCTTGTGTGTGTGAGCTGCCATAG 900
DB 841 CGATGGCAAGAGGCTGAGAGTGTCTGTGACAAAGTCTTGTGTGTGTGAGCTGCCATAG 900
OY 901 GATTTGGCTGGACAGCTGATCATCCAGCTGAGGGCTACGCCATAGCTTGTGAGTGG 960
DB 901 GATTTGGCTGGACAGCTGATCATCCAGCTGAGGGCTACGCCATAGCTTGTGAGTGG 960
OY 961 GCATGGCCCACTACAGATAGAGGAGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
DB 961 GCATGGCCCACTACAGATAGAGGAGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
OY 1021 GCTCAATTTCTCAAGGCAACAGAGTGGAGGCACTGAGAGGGGCTCATGTGTGT 1080
DB 1021 GCTCAATTTCTCAAGGCAACAGAGTGGAGGCACTGAGAGGGGCTCATGTGTGT 1080
OY 1081 ACCCAGGG 1140

DB 1081 ACCCAGGG 1140
OY 1141 GACTGACATACCTGACATGTAGTAGAGGCTGTGGGTGAGAGTGTATGTGTGTAT 1200
DB 1141 GACTGACATACCTGACATGTAGTAGAGGCTGTGGGTGAGAGTGTATGTGTGTAT 1200
OY 1201 GGGCAGGCGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
DB 1201 GGGCAGGCGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
OY 1261 GGGAGTGAACCTATCTGTGTGACAGAGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
DB 1261 GGGAGTGAACCTATCTGTGTGACAGAGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
OY 1321 ATTACCCCACTTGTGAGTGAAGAACTTATATGAAGCAAGTGTGTGTGTGTGTGTGTGT 1380
DB 1321 ATTACCCCACTTGTGAGTGAAGAACTTATATGAAGCAAGTGTGTGTGTGTGTGTGTGT 1380
OY 1381 TGAACCACTACCTTGTGTGAGGAGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
DB 1381 TGAACCACTACCTTGTGTGAGGAGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
OY 1441 CTCAGAGGAGTGAAGCCTTGTCAACAGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
DB 1441 CTCAGAGGAGTGAAGCCTTGTCAACAGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
OY 1501 CACCTTGTGAGTGAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
DB 1501 CACCTTGTGAGTGAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
OY 1561 CAATGTGTCCCACTGCAAGATGATGACAAACCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
DB 1561 CAATGTGTCCCACTGCAAGATGATGACAAACCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
OY 1621 CAGAGAGGCGCTTGT 1680
DB 1621 CAGAGAGGCGCTTGT 1680
OY 1681 TACCTACCCCTTGT 1740
DB 1681 TACCTACCCCTTGT 1740
OY 1741 AAGCTCTTGT 1800
DB 1741 AAGCTCTTGT 1800
OY 1801 AAGGCTGAGT 1860
DB 1801 AAGGCTGAGT 1860
OY 1861 GCTGAGGAGT 1920
DB 1861 GCTGAGGAGT 1920
OY 1921 GTGCTATTTGT 1980
DB 1921 GTGCTATTTGT 1980
OY 1981 ACATTTGATTT 2040
DB 1981 ACATTTGATTT 2040
OY 2041 TCTGT 2100
DB 2041 TCTGT 2100
OY 2101 AAAAGAGCAAGCTGT 2160
DB 2101 AAAAGAGCAAGCTGT 2160
OY 2161 TGCATTAATCAATGAGT 2220

1141 GACTGCATACCTGACATGGTAGTAGAGCCCTGTGGGTGAGTTAGTCTATGCTGTGGTAT 1200
1141 GACTGCATACCTGACATGGTAGTAGAGCCCTGTGGGTGAGTTAGTCTATGCTGTGGTAT 1200

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OY 1201 GGGGAGCCCAAGGTTGCAATGGGAAAAACAGCCCTACAGAGTGCATCTTGGAGAGA 1260
Db 1201 GGGGAGCCCAAGGTTGCAATGGGAAAAACAGCCCTACAGAGTGCATCTTGGAGAGA 1260
OY 1261 GGGGAATACCTCATCTCTCCAGAAATGGGAGTCCCTCTTCTAGAGATCTTATGAA 1320
Db 1261 GGGGAATACCTCATCTCTCCAGAAATGGGAGTCCCTCTTCTAGAGATCTTATGAA 1320
OY 1321 ATTACCCACCTTGTGATGAAAGAACCTTATTAAGCAAGTCACTGTGCATCTTCC 1380
Db 1321 ATTACCCACCTTGTGATGAAAGAACCTTATTAAGCAAGTCACTGTGCATCTTCC 1380
OY 1381 TGACCACTACCTCTTCTTCTAGGCAATGTCATCCCGCTAGTCATCCCGCTAGCCCA 1440
Db 1381 TGACCACTACCTCTTCTTCTAGGCAATGTCATCCCGCTAGTCATCCCGCTAGCCCA 1440
OY 1441 CTCGAGGAGCTCAGACCCATCTCCAGCAGTGCATGCTTCCAGCAAGA 1500
Db 1441 CTCGAGGAGCTCAGACCCATCTCCAGCAGTGCATGCTTCCAGCAAGA 1500
OY 1501 CACCTTACCTACCTTATTAAGACCCCATTAACCACTATGCTTCTCTTCTACT 1560
Db 1501 CACCTTACCTACCTTATTAAGACCCCATTAACCACTATGCTTCTCTTCTACT 1560
OY 1561 CAATGCTCCCACTCAGATGATGACACAAACCCCTGCCCCCAATTTTGGAGATCC 1620
Db 1561 CAATGCTCCCACTCAGATGATGACACAAACCCCTGCCCCCAATTTTGGAGATCC 1620
OY 1621 CAGAGAGGAGGCTTCTTGTGATTCACCAAGTTTATGATCAGTCTGCCCAAAATAGAGCT 1680
Db 1621 CAGAGAGGAGGCTTCTTGTGATTCACCAAGTTTATGATCAGTCTGCCCAAAATAGAGCT 1680
OY 1681 TACCTACCCCTCTTCTTGTGAGACCCCTGCTCTTCTTCTTCTTCTTCTTCTTCT 1740
Db 1681 TACCTACCCCTCTTCTTGTGAGACCCCTGCTCTTCTTCTTCTTCTTCTTCTTCT 1740
OY 1741 AAGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1800
Db 1741 AAGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1800
OY 1801 AAGGGGTGACTTGCCTGAGCTCTATCAGCTGAGCTCCCTGCTGCTCTCTCTCTCT 1860
Db 1801 AAGGGGTGACTTGCCTGAGCTCTATCAGCTGAGCTCCCTGCTGCTCTCTCTCTCT 1860
OY 1861 GGTGAGGAGATTTCTTATCCCTGCTCTCTCTGCTAGGTGCTAGTCTGCTGACT 1920
Db 1861 GGTGAGGAGATTTCTTATCCCTGCTCTCTCTGCTAGGTGCTAGTCTGCTGACT 1920
OY 1921 GTGCTATTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
Db 1921 GTGCTATTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
OY 1981 ACATTTCTGATTTTTTTTTTTTTTTTTTTTTTGAAGATTAATAATCTTAATTTTAT 2040
Db 1981 ACATTTCTGATTTTTTTTTTTTTTTTTTTTTTGAAGATTAATAATCTTAATTTTAT 2040
OY 2041 TCTGTGATCTACAGCAATTAAGGCAATATACCTGATGATGATGATGATGATGATGAT 2100
Db 2041 TCTGTGATCTACAGCAATTAAGGCAATATACCTGATGATGATGATGATGATGATGAT 2100
OY 2101 AAAAGCAAAAGCTACAAAGATTAAGAGCTCAGAAATGATGATGATGATGATGATGAT 2160
Db 2101 AAAAGCAAAAGCTACAAAGATTAAGAGCTCAGAAATGATGATGATGATGATGATGAT 2160
OY 2161 TGCATTAATCAATAGTGCATCTTTTGAAGCTGTGCTATGACAGTCTCTGAAGAAAG 2220
Db 2161 TGCATTAATCAATAGTGCATCTTTTGAAGCTGTGCTATGACAGTCTCTGAAGAAAG 2220
OY 2221 GGTTCCTGTTTAAAGCTGAGTAACTTTCTGATGATGATGATGATGATGATGATGAT 2272
Db 2221 GGTTCCTGTTTAAAGCTGAGTAACTTTCTGATGATGATGATGATGATGATGATGAT 2272

```

RESULT 5

US-08-482-577B-3

Sequence 3, Application US/08482577B

Patent No. 5807713

GENERAL INFORMATION:

APPLICANT: HOTTEN, GERTRUD

APPLICANT: NEIDHARDT, HELGE

APPLICANT: BECHTOLD, ROLF

APPLICANT: POHL, JENS

TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL

TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

STREET: 655 FIFTEENTH STREET, N.W., C STREET LOBBY,

STREET: SUITE 330

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,577B

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KLESNER, SHARON

REGISTRATION NUMBER: 36,335

REFERENCE/DOCKET NUMBER: P564-5010

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1558 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

PUBLICATION INFORMATION:

DOCUMENT NUMBER: US 08/289,222

FILING DATE: 12-AUG-1994

US-08-482-577B-3

Query Match 34.4%; Score 781; DB 1; Length 1558;

Best Local Similarity 79.9%; Pred. No. 5, 1e-189;

Matches 959; Conservative 0; Mismatches 235; Indels 7; Gaps 3;

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OY 24 CACACTTCTCCAGGGGCTTGTGAGAGCCGAGAGAGTGAAGACAGCTGTTGAGACC 83
Db 28 CACACTTCTCCAGGGGCTTGTGAGAGCCGAGAGAGTGAAGACAGCTGTTGAGACC 86
OY 84 CTGAGCCCTGAGTCTGATTTGCTCAAGAAAGGCTTCCCAAGCAATGACTCTCTATTC 143
Db 87 CTGAATATAGCGTTTGGGCTTGAAGAGGCTATCTCCAGCAATGAGCTCTCTATTC 146
OY 144 TTCTGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 203
Db 147 TCTGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 206
OY 204 GTCAGCATGTGGGGGAGCCACCTTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 263
Db 207 GCCAGCATGTGGGGGAGCCACCTTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 266
OY 264 TGGCAAGAGAGAGATCTTGAGACAGCTGACCTCACCAGGAGAGAGAGAGAGAGAGAG 323
Db 267 TGGCAAGAGAGAGATCTTGAGACAGCTGACCTCACCAGGAGAGAGAGAGAGAGAGAG 326

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Db 121 CACAGCTGAGGACCACTGAGGGGGCTCATGCTGTGTACCCAGGCCGCCGCCCT 180
Qy 1102 GTCCTGCTATTTATGACAGGACAGACATGTGTACAGCTGACATACCTGATGTT 1161
Db 181 GTCCTGCTATTTATGACAGGACAGACATGTGTACAGCTGACATACCTGATGTT 240
Qy 1162 AGTAGAGGCTGTGGTGCAGTTAG 1186
Db 241 AGTAGAGGCTGTGGTGCAGTTAG 265

RESULT 8

US-09-054-526B-5
Sequence 5, Application US/09054526B
Patent No. 6197550
GENERAL INFORMATION:
APPLICANT: H TREN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAI DO, MARCELSTEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,526B
FILING DATE: 03-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-8005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA from mRNA
US-09-054-526B-5

Query Match 11.7%; Score 265; DB 4; Length 265;
Best Local Similarity 100.0%; Pred. NO. 2.7e-58;

Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 922 CATCAGCCTGAGGCTAGCCATGACTTGTGATAGGCGAGTGCACCTAGACATAGC 981

Db 1 CATCAGCCTGAGGCTAGCCATGACTTGTGATAGGCGAGTGCACCTAGACATAGC 60
Qy 982 AGGCATGCTGGTATATGCTGCTCTTTCACACTGAGTGCCTCAATCTCTCAAGGCCAA 1041
Db 61 AGGCATGCTGGTATATGCTGCTCTTTCACACTGAGTGCCTCAATCTCTCAAGGCCAA 120
Qy 1042 CACAGCTGAGGACCACTGAGGGGGCTCATGCTGTATACCCAGGCCGCCGCCCT 1101
Db 121 CACAGCTGAGGACCACTGAGGGGGCTCATGCTGTATACCCAGGCCGCCGCCCT 180
Qy 1102 GTCCTGCTATTTATGACAGGACAGACATGTGTACAGCTGACATACCTGATGTT 1161
Db 181 GTCCTGCTATTTATGACAGGACAGACATGTGTACAGCTGACATACCTGATGTT 240
Qy 1162 AGTAGAGGCTGTGGTGCAGTTAG 1186
Db 241 AGTAGAGGCTGTGGTGCAGTTAG 265

RESULT 9

US-08-455-550-2
Sequence 2, Application US/08455550
Patent No. 5670338
GENERAL INFORMATION:
APPLICANT: MURAKAMI, KAZUO
APPLICANT: KATO, YUKIO
APPLICANT: UENO, NAOTO
TITLE OF INVENTION: XENOPUS LAEVIS BONE MORPHOGENETIC PROTEINS AND USE THE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, Bronstein, Roberts & Cushman
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,550
FILING DATE: 31-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/056,564
FILING DATE: 30-APR-1993
APPLICATION NUMBER: 07/577,892
FILING DATE: 05-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 40302-FWC-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-455-550-2

Query Match 6.3%; Score 142.4; DB 1; Length 687;

TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...357
OTHER INFORMATION:
US-08-765-662-11

Query Match 6.2%; Score 140.2; DB 2; Length 360;
Best Local Similarity 65.3%; Pred. No. 1.6e-26;
Matches 224; Conservative 0; Mismatches 113; Indels 6; Gaps 1;

QY 844 CTGCCAAGAGGAGGCTCCAGATGTCGTGTCGACAGAGATTGTTGTGACTTCCTGAGAT 903
DB 24 CTGTGAGCCTCGACCCCTTATGTTGACAGGAGACCATTAAGTACCTCCAGAACT 83
QY 904 TGCGTGCAGAGCTGATGATCATCCAGCCTGAGGGCTACGCCATGAATCTGCTAGAGCA 963
DB 84 GGGATGGCGGAGCTGATGATCATCCAGCCTGAGGGCTACGCCATGAATCTGCTAGAGCA 143
QY 964 GTGCCACTACATACATACAGGAGGCTGATGATGCTGCTGCTTTCACACTGCAAGTCT 1023
DB 144 GTGCCCTCCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203
QY 1024 CAATCTTCTCAAGGCCAACAACAGCTGAGGAGGCTGCTGCTGCTGCTGCTGCTGCT 1083
DB 204 CAGCCTCTCAAGGCCAACAACAGCTGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 257
QY 1084 CAGGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143
DB 258 TACTGCCCGAAGGCCCT 317
QY 1144 TGACATACCTGACATGATAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1186
DB 318 GGATGTGCCAGATATGCTGTGAGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

RESULT 12
US-09-184-933-11
Sequence 11, Application US/09184933
Patent No. 6130050
GENERAL INFORMATION:

APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/184,933
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/274,215
FILING DATE: 13-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5039
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...357
US-09-184-933-11

Query Match 6.2%; Score 140.2; DB 3; Length 360;
Best Local Similarity 65.3%; Pred. No. 1.6e-26;
Matches 224; Conservative 0; Mismatches 113; Indels 6; Gaps 1;

QY 844 CTGCCAAGAGGAGGCTCCAGATGTCGTGTCGACAGAGATTGTTGTGACTTCCTGAGAT 903
DB 24 CTGTGAGCCTCGACCCCTTATGTTGACAGGAGACCATTAAGTACCTCCAGAACT 83
QY 904 TGCGTGCAGAGCTGATGATCATCCAGCCTGAGGGCTACGCCATGAATCTGCTAGAGCA 963
DB 84 GGGATGGCGGAGCTGATGATCATCCAGCCTGAGGGCTACGCCATGAATCTGCTAGAGCA 143
QY 964 GTGCCACTACATACATACAGGAGGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCT 1023
DB 144 GTGCCCTCCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203
QY 1024 CAATCTTCTCAAGGCCAACAACAGCTGAGGAGGCTGCTGCTGCTGCTGCTGCTGCT 1083
DB 204 CAGCCTCTCAAGGCCAACAACAGCTGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 257
QY 1084 CAGGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143
DB 258 TACTGCCCGAAGGCCCT 317
QY 1144 TGACATACCTGACATGATAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1186
DB 318 GGATGTGCCAGATATGCTGTGAGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

RESULT 13
PCT-US95-08745-11
Sequence 11, Application PC/TUS9508745
GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08745
FILING DATE: 12-JUL-1995
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Hallie, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/042N01 (FD-3830)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..357
OTHER INFORMATION:
DCT-US95-08745-11

STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08745
FILING DATE: 12-JUL-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/042M01 (FD-3830)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2419 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 218..1267
OTHER INFORMATION:
PCT-US95-08745-13

Query Match 6.2%; Score 140.2; DB 5; Length 2419;
Best Local Similarity 65.3%; Pred. No. 3.6e-26;
Matches 224; Conservative 0; Mismatches 113; Indels 6; Gaps 1;
QY 844 CTGCCAAGGAGGGGTCCAGATGCTGTGACAGAGTTTGTGGACTCCGTGAGAT 903
DB 934 CTGTGAGCCTGGCGACCCCTTATGTTCAGGCGAGCCATTACGTGACTTCCAGGACT 993
QY 904 TGGCTGGCAGCAGTGCATCCAGCCTGAGGGCTACGCCATGAACCTTCTGCATAGGGCA 963
DB 994 GGGATGGCGGGAGTGCATGCTGACGCCGAGGGGTACAGCTGAATTACTGCAGTGGGCA 1053
QY 964 GTGCCCACTACACATAGCAGGATGGCTGATGTGCTGCTCTTTCACACTGCAGTGT 1023
DB 1054 GTGCCCTCCCACTGGCTGGCAGCCAGCCAGCATGTGCTGCTTTCATTCATTCGCCCTTT 1113
QY 1024 CAATCTTCTCAAGCCACACAGCTGCAGGACCACTGGAGGGGCTCATGCTGTATCC 1083
DB 1114 CAGCCTCTCAAGCCACCAATCCT-----TGGCTGCAGATACCTCTCTGTGTCTCC 1167
QY 1084 CAGGCGCCGCCCTCTCTCTCTCTATATATGACAGGACAGCAACATTTGTCAGAC 1143
DB 1168 TACTGCCCCAGAGCCCTCTCTCTCTACCTGCATCATATGCAATGTGTCAGAC 1227
QY 1144 TGACATACCTGACATGTGTAGAGGCGGTGGGTGCAGTTAG 1186
DB 1228 GGATGTGCCAGATATGTGTGTGAGAGCCGTGTGCTGCAGCTAG 1270

Search completed: October 11, 2002, 22:15:16
Job time : 64.7958 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2002, 22:15:08 : Search time 1835.4 Seconds
(Without alignments)
16707.608 Million cell updates/sec

Title: US-09-684-383-1
Perfect score: 2272
Sequence: 1 CAAGGACGATCCAGCTG.....ACTATGATCATCTTCCTT 2272

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estdb:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	738.2	32.5	1011	11	BC020693 Homo sapi
2	499.4	22.0	541	10	BC566943 602589447
3	418	18.4	758	10	BI328115 602979264
4	416.8	18.3	893	10	BI246740 602959660
5	404.8	17.8	829	10	BI329959 602980519
6	401.2	17.7	823	10	BF533960 602075120
7	399	17.6	841	10	BI145698 602909844
8	396	17.4	941	10	BI148079 602912428
9	378	16.6	816	10	BF232704 602023292
10	369.2	16.2	975	10	BF533968 602075129
11	283.2	12.5	594	9	AV658436
12	283.2	12.5	1113	10	BM463852
13	281.4	12.4	475	10	BC084513
14	280	12.3	589	10	BI986860
15	279.4	12.3	567	10	BC801734 0114-08 M
16	279	12.3	329	10	BF455465 UI-M-B21-
17	279	12.3	359	10	BF455462 UI-M-B21-

18	279	12.3	404	10	BE852372	BE852372 uv19e06.x
19	279	12.3	440	10	BE996475	BE996475 UI-M-GCOP
20	279	12.3	644	10	BC684918	BC684918 60263653
21	278.4	12.3	585	12	A2795923	A2795923 2M0051822
22	276.4	12.2	420	10	BF662934	BF662934 602144726
23	276.4	12.2	513	10	BI398655	BI398655 MI-P-AV1-
24	276	12.1	376	10	BF151003	BF151003 uy90h04.x
25	276	12.1	568	10	BF972653	BF972653 602243092
26	275.8	12.1	346	9	BE133911	BE133911 u906e07.x
27	275	12.1	506	10	BI695500	BI695500 603344811
28	274	12.1	347	9	AA620486	AA620486 ae0b02.s
29	273.4	12.0	537	10	BF791596	BF791596 602251716
30	273	12.0	522	9	AI954151	AI954151 vx80d04.x
31	272.8	12.0	549	10	BI499054	BI499054 1e2b02.x
32	272.4	12.0	586	9	AA209153	AA209153 u002f01.x
33	272.2	12.0	475	10	BE991905	BE991905 UI-M-B21-
34	271.4	11.9	443	9	AI201615	AI201615 qb81c01.x
35	268	11.8	390	10	BF660636	BF660636 ma82e06.
36	268	11.8	479	9	AA029894	AA029894 zk08f02.s
37	268	11.8	631	10	BM272210	BM272210 1g40f09.x
38	267	11.8	285	9	AA183246	AA183246 m82807.r
39	267	11.8	443	10	BF109198	BF109198 715b811.x
40	267	11.8	598	10	BF684212	BF684212 602141120
41	266.4	11.7	358	9	AA011197	AA011197 z623c01.s
42	266.4	11.7	603	9	AU143968	AU143968 AU143968
43	266	11.7	348	9	AA268442	AA268442 vx40b05.x
44	266	11.7	714	10	BI861129	BI861129 603390870
45	265.4	11.7	583	9	AA877215	AA877215 ob15e02.s

ALIGNMENTS

RESULT 1
LOCUS BC020693 1011 bp mRNA linear HTC 22-JAN-2002
DEFINITION Homo sapiens, similar to inhibin, beta C, clone IMAGE:4723762,
mRNA.

ACCESSION BC020693.1 GI:18088855
VERSION HTG.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 1011)
JOURNAL Direct Submission
Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgaphs-r@mail.nih.gov

Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcddpaxll.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNI at: <http://imgc.ilni.gov>
Series: IRL Plate: 37 Row: g Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA g1: 15718678
This clone has the following problem: frame shifted.

FEATURES
source 1..1011
Location/Qualifiers

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4723762"
/tissue_type="Liver"
/lab_host="NIH-MGC-76"
/lab_host="DH10B"
/notes="Vector: pDNR-LIB"
BASE COUNT      271 a      276 c      243 g      221 t
ORIGIN

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Query Match      32.5% Score 738.2; DB 11; Length 1011;
Best Local Similarity 99.5%; Pred. No. 4.4e-105;
Matches 751; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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```

OY 1 CAAGGAGCCATGTCAGTGGACACACATCTTCCAGGCGCTTGGCAGCAGACAGAG 60
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DB 17 CAAGGAGCCATGTCAGTGGACACACATCTTCCAGGCGCTTGGCAGCAGACAGAG 76
OY 61 TTGAGACACAGCTGTTGAGACCCCTGAGCTGATGCTAATGCTCAAGAGGCGCTTC 120
    |||
DB 77 TTGAGACACAGCTGTTGAGACCCCTGAGCTGATGCTAATGCTCAAGAGGCGCTTC 136
OY 121 CCAGCAATACCTCTCTCATCTGCTTCTGGCC-TTTCTCTCTGCTCCACACAGTGG 179
    |||
DB 137 CCAGCAATACCTCTCTCATCTGCTTCTGGCC-TTTCTCTCTGCTCCACACAGTGG 196
OY 180 CCACTCCACAGCTGGCGGTCACTGTCAGCATGTGGGGGCCACCTTGGAACTGGAGA 239
    |||
DB 197 CCACTCCACAGCTGGCGGTCACTGTCAGCATGTGGGGGCCACCTTGGAACTGGAGA 256
OY 240 GCCAGGGGAGCTGCTTCTTGTATCTGCGCAAGAGACATCTTGGACAACTGACCTCA 299
    |||
DB 257 GCCAGGGGAGCTGCTTCTTGTATCTGCGCAAGAGACATCTTGGACAACTGACCTCA 316
OY 300 CCCAGGGGCCCAACACTGAAACCGCCCTGTGTCCAGAGCTGTTGAGAGCTGCACTGACG 359
    |||
DB 317 CCCAGGGGCCCAACACTGAAACCGCCCTGTGTCCAGAGCTGTTGAGAGCTGCACTGACG 376
OY 360 ACCTCCACAGGGGTCCACAGGGGGGCACTTCTAGAGGACAAACAGGAAAGATGTGAA 419
    |||
DB 377 ACCTCCACAGGGGTCCACAGGGGGGCACTTCTAGAGGACAAACAGGAAAGATGTGAA 436
OY 420 TCATGAGCTTGTGAGACAGGCTTCTCCACATCAACAGAGCTGCTTGTATTTTCACT 479
    |||
DB 437 TCATGAGCTTGTGAGACAGGCTTCTCCACATCAACAGAGCTGCTTGTATTTTCACT 496
OY 480 TCCTCTCTGATGAACACTGCTGTGTGACAGGAGGTCAGCAGGACCACTCATGTTCTTG 539
    |||
DB 497 TCCTCTCTGATGAACACTGCTGTGTGACAGGAGGTCAGCAGGACCACTCATGTTCTTG 556
OY 540 TGGAGCTCCCTTCCATACCACTTGGACCTTGAAGTGAGAGCTCTTGTGCTGGCTCAC 599
    |||
DB 557 TGGAGCTCCCTTCCATACCACTTGGACCTTGAAGTGAGAGCTCTTGTGCTGGCTCAC 616
OY 600 ATAAATACCAACCTGACCTTGGCTACTAGTACCTGCTGAGAGTGATGCAATGGCTGGC 659
    |||
DB 617 ATAAATACCAACCTGACCTTGGCTACTAGTACCTGCTGAGAGTGATGCAATGGCTGGC 676
OY 660 ATCAACTCCCTTCCAGGCTGTAAGCTCAAGCTGACAGCCAGGAGGCACTTGACCTTGG 719
    |||
DB 677 ATCAACTCCCTTCCAGGCTGTAAGCTCAAGCTGACAGCCAGGAGGCACTTGACCTTGG 736
OY 720 AGCTGCTACTTGAAGGCCAGAGTGAAGCCCAAGAGCTCA 754
    |||
DB 737 AGCTGCTACTTGAAGGCCAGAGTGAAGCCCAAGAGTCA 771

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```

RESULT 2
LOCUS      BG566943
DEFINITION 60289447p1 NIH-MGC-76 Homo sapiens cDNA clone IMAGE:4723762 5'
ACCESSION  BG566943

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VERSION      BG566943.1 GI:13574596
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    NIH-MGC http://mhc.ncl.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE        Unpublished (1999)
JOURNAL      Contact: Robert Strausberg, Ph.D.
COMMENT      Email: cga@b-remail.nih.gov
              Tissue Procurement: CLONTECH Laboratories, Inc.
              cDNA Library Preparation: CLONTECH Laboratories, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              http://image.llnl.gov
              Plate: LCM1583 row: m column: 11
              High quality sequence stop: 539.

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FEATURES
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        Location/Qualifiers
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                /db_xref="taxon:9606"
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                /lab_host="NIH-MGC-76"
                /note="Organ: Liver; Vector: pDNR-LIB (Clontech); Site_1:
                SfiI (ggcgccgcgcgcgc); Site_2: SfiI (ggcattatggcc); 5' and
                3' adaptors were used in cloning as follows: 5' adaptor
                sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence:
                5'-ATTCAGAGCGCGGAGGCGCCAGATG-dt(30)BN-3' (where B = A,
                C, or G and N = A, C, G or T). Average insert size 1.85
                kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
                by PCR. This library was enriched for full-length clones
                and was constructed by Clontech Laboratories (Palo Alto,
                CA). Note: this is a NIH-MGC Library."

```

```

BASE COUNT      117 a      172 c      143 g      109 t
ORIGIN

```

```

Query Match      22.0% Score 499.4; DB 10; Length 541;
Best Local Similarity 99.4%; Pred. No. 5.4e-68;
Matches 522; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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```

OY 1 CAAGGAGCCATGTCAGTGGACACACATCTTCCAGGCGCTTGGCAGCAGACAGAG 60
    |||
DB 18 CAAGGAGCCATGTCAGTGGACACACATCTTCCAGGCGCTTGGCAGCAGACAGAG 77
OY 61 TTGAGACACAGCTGTTGAGACCCCTGAGCTGATGCTAATGCTCAAGAGGCGCTTC 120
    |||
DB 78 TTGAGACACAGCTGTTGAGACCCCTGAGCTGATGCTAATGCTCAAGAGGCGCTTC 136
OY 121 CCAGCAATACCTCTCTCATCTGCTTCTGGCC-TTTCTCTCTGCTCCACACAGTGG 179
    |||
DB 137 CCAGCAATACCTCTCTCATCTGCTTCTGGCC-TTTCTCTCTGCTCCACACAGTGG 196
OY 180 CCACTCCACAGCTGGCGGTCACTGTCAGCATGTGGGGGCCACCTTGGAACTGGAGA 239
    |||
DB 197 CCACTCCACAGCTGGCGGTCACTGTCAGCATGTGGGGGCCACCTTGGAACTGGAGA 256
OY 240 GCCAGGGGAGCTGCTTCTTGTATCTGCGCAAGAGACATCTTGGACAACTGACCTCA 299
    |||
DB 257 GCCAGGGGAGCTGCTTCTTGTATCTGCGCAAGAGACATCTTGGACAACTGACCTCA 316
OY 300 CCCAGGGGCCCAACACTGAAACCGCCCTGTGTCCAGAGCTGCTTGAAGAGTGAAGTGA 359
    |||
DB 317 CCCAGGGGCCCAACACTGAAACCGCCCTGTGTCCAGAGCTGCTTGAAGAGTGAAGTGA 376
OY 360 ACCTCCACAGGGGTCCACAGGGGGGCACTTGAAGAGCAACAGGAGCAAGATGTGAA 419
    |||
DB 377 ACCTCCACAGGGGTCCACAGGGGGGCACTTGAAGAGCAACAGGAGCAAGATGTGAA 436

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Technologies. Note: this is a NCI_CGAP Library.
 BASE COUNT 196 a 259 c 242 g 196 t

Query Match 18.3% Score 416.8; DB 10; Length 893;
 Best Local Similarity 74.7%; Pred. No. 2.7e-55;
 Matches 644; Conservative 0; Mismatches 202; Indels 16; Gaps 9;

96 TCTGTATTTGTCAGAGAGGCGCTTCCACACATAGACCTCTGCTGCGCTTC 155
 5 TTTGGGCTCTTTAAGAGAGCTATCTCCACAGAAAGGCTCTCTGCTGCGCTTC 64
 156 TCTCTGCTGCTCCAGACAGTGGCCACTCCAGAGCTGGCGCTGCTGCTGCTG 215
 65 TGTCTGCTGCTCCAGACAGTGGCCACTCCAGAGCTGGCGCTGCTGCTGCTG 124
 216 GGGGCGCCACTTGGAGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 275
 125 GGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 184
 276 GCATCTTTGACAGAGCTGACCTGACCCAGGCGCCAGACACTGAGGCGCTG 335
 185 GTATCTGCTGAGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 244
 336 CTGCTTTGAGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAG 394
 245 GGGGCTGCTGAGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 304
 395 -GACAAACAG 452
 305 ATGACAG 364
 453 TCACACAG 512
 365 TCACACAG 422
 513 TCCAG 572
 423 TCCAG 482
 573 AAGTGAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632
 483 ATATAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
 633 T-GCTGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGG 691
 543 TGGTTCAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGG 602
 692 GCGTGAAG 749
 603 GCGTGAAG 662
 750 GCTGAGTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 809
 663 GTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 722
 810 GGGG-----CAAAACAGAGATTCACGAGAGAGAGAGAGAGAGAGAGAG 863
 723 GAGGGGCAAG 782
 864 -TGTGCTGCTGAG 921
 783 TTTGCTGCTGAG 842
 922 CATCCAG 943
 843 CATCCAG 864

RESULT 5 B1329959 829 bp mRNA linear EST 30-JUL-2001
 LOCUS B1329959
 DEFINITION 602980519p1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5133317 5'

ACCESSION mRNA sequence.
 B1329959
 VERSION B1329959.1 GI:15014616
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 829)
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
 http://image.jnl.gov
 Plate: LAM11327 row: F column: 06
 High quality sequence stop: 789.
 Location/Qualifiers
 1..829
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 /strain="FVB/N"
 /db_xref="taxon:10090"
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 /clone_11b="NCI_CGAP_L19"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: Liver; Vector: pCMV-Sport6; Site: 1; NCI; Site-2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 197 a 246 c 217 g 179 t

Query Match 17.8% Score 404.8; DB 10; Length 829;
 Best Local Similarity 74.9%; Pred. No. 2e-53;
 Matches 574; Conservative 0; Mismatches 182; Indels 10; Gaps 5;

24 CACACTTCTCCAGAGGCTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 83
 49 CACATTTCTCCAGAGGCTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 108
 84 CTGAGCCCTGAGTCTGATTTCTCAAGAGAGGCTTCCCAAGATGACCTCTCAT 143
 109 CTGAATATAGGCTTTGGCTCTTTAAGAGAGGCTATCTCCAGCAATGAGCTCT 168
 144 TTTGAGCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203
 169 TCTGCGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 228
 204 GTCCAGATGTTGGGGGCGCCACTTGGAACTGAGAGAGAGAGAGAGAGAGAG 263
 229 GCCAGAGATTTGGGGGCGCCACTTGGAACTGAGAGAGAGAGAGAGAGAGAG 288
 264 TGGGCAAG 323
 289 TGGCAAG 348
 324 CTGTGCTCAGAGTGTCTTGGAGAGTCACTGAGAGAGAGAGAGAGAGAGAGAG 383
 349 CAGTGTCCAGAGGGGCTCTCAAGAGCCGCTGAGAGCCCTCCGCGGCTTGAAG 408
 384 CACTTCTAGAG--GACAAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 440
 409 CCGTGAAG 468
 441 GCGTCTCAG 500
 469 ACCTCTCAGAGATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 525

OY 501 GTGACAGGAGAGTCCAGACGACCGCATCTAGTCTCTTGTGTACACTCCCTTCCAAATACA 560
 Db 526 GTGGCATGAGAGTCCGGCAGACCCGCTTACATGTTCTTGTCACATGTCCCCCAACATGCA. 585
 OY 561 CTYGGACCTTGAAGTGAGAGTCTCTTGTGCTGGGTCCACATTAATACCACTCACTTGG 620
 Db 586 CCCAGACCATCAATTAATAGAGTCTTGTGTCTAAGCACCATAGACAGCAA.-TTCACCTTTGA 644
 OY 621 CTACTCAGTACTCGTGTGGAGGTGATGTGCACAGGCTGCATCACTCCCTTAGGGCTG 680
 Db 645 CAAGTCACTACTGTTGGTGCAGGTGAATGCCAGTGG.-TGGTACCAGAGTTCTCCGTGGGACTG 703
 OY 681 AAGCTCAAGCTCCCTGCACGCCAGGGGCACTTCAGCTCGAGCTGTACTTGAAGGCCAGG 740
 Db 704 AAGCTCAAGCTCTTGCAGGCCATGCACACCTTAACCTGAGAGTGGTATACACAGAAAGC.-AG 761
 OY 741 TAGCCAGAGCTCAGTCATCCTGGGTGAGAGCTGCCCATAGGCTTT 786
 Db 762 GTGGCCACAGTACCTTGAATCCTTGGGCTGGTTTACCACAGAGGCTTT 807

RESULT 6	823 bp	mRNA	linear	EST 11-DEC-2000
BF533960				
LOCUS				
602075120F1	NCI_CGAP_L19	MUS	MUSCULUS	CDNA
DEFINITION				clone IMAGE:421225 5' ,
	mRNA sequence,			

ACCESSION	BF533960
VERSION	BF533960.1
	GI:11621323

KEYWORDS	EST.
SOURCE	house mouse
ORGANISM	Mus musculus

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Mus musculus	Mammalia: Mammalia: Chordata: Craniata: Vertebrata: Euteleostomi: Eukaryota	Mammalia: Eutheria: Rodentia: Sclerognathi: Muridae: Murinae: Mus	1 (bases 1 to 82)	Nih-MGC http://mgc.ncl.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)
	Unpublished (1999)				Contact: Robert Strausberg, Ph.D.

Email: cgabos-remail@att.net
Tissue Procurement: Jeffrey E. Green, M.D.,
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LLAM0782 row: 9 column: 06
high quality sequence stop: 754.

FEATURES
source

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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4212125"
/clone_1lb="NCL_GCAP_L19"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: Liver; Vector: pCMV-SPO86; Site_1: NCL; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCL_GCAP Library."

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Query Match	17.7%	Score 401.2;	DB 10;	Length 823;
Best Local Similarity	75.3%	Pred. No. 7.2e-53;		
Matches 593;	Conservative 0;	Mismatches 183;	Indels 12;	Gaps 7
QY	43	CTGCAGCCAGACAGAGCTGTGAGACCAAGCTGTTGAACCTTGAGCCCTGAGCTCTGAT	102	
DB	5	CTGTGTCGCCAGACAGAGCTGTGAGCCATCCCGTTGAGAACCTCGA-ATATAGGCTTGCGT	63	
QY	103	TGCTCAAGAGGGCTTCCGCCAGCAATACCTCCATCTGCTTGCGGCTTCTCTCTCT	162	

Db 64 CTTTAAAGGAGGCTATCTCTCAGCAATGGCGCTCTCTCTTGGCTCTGCTGTTGCTT 123
 Oy 163 GGCCTCAACCAACAGTGGCCACTCTCCAGAGCTGGCGGTTCAGTGTCCACATATGTGGGGGCC 222
 Db 124 GACTTCACACCACTAGTGAACCCCAAAACTGAGGGTGCATGAGCCACATGTGGGGTGC 183
 Oy 223 CACCTTGGAACTGAGACCCAGGGGGAGCTCTTTCTTGATCTGGCCAAAGACATCTT 282
 Db 184 CATCTTCACTCGGAGACCCAGCGGAGCTCTCTTGAT -TGGCCAAAGAAAGTATTCCT 242
 Oy 283 GCACAGCTGCACCTCCACCCAGCGGCCCAACAGTAAACCGCCCTGTGTCCAGAGCTGCTT 342
 Db 243 GGACAAAGTGCACCTCAGCCAGCGGCCCATACTCAGTGGCCAGTGTTCACAGAGGGGCTCT 302
 Oy 343 GAGACCTGCACCTGCAGCACCTTCACGGGGTCCCAAGGGGGCACTTCTAGAG---GACAA 399
 Db 303 CAAGACCGGGCTGCAGCGCCCTCCGGGGCTTCGACAGGGAAACCTGTGGTGAACATGACCA 362
 Oy 400 CAGGGACAGGAATGTGAATATCATCAGCTTGTGTGAGACAGAGCCCTCCACCATCAACCA 459
 Db 363 GAGACAAAGAAATATGATGATCATCAGCTTGTGTGACACAGACCTCCACACATCAACCA 422
 Oy 460 GACTCGCTTGAATTTCACTTCTCCTCTGTATGAACCTGCTGTACAGGAGGTCCACCA 519
 Db 423 GACCCGGCTCGAGTTTCCACT--CTGTGTGAATATGGCCAACTGGCATGAGAGTCCGCCA 479
 Oy 520 GGCACGCTCATGTTCTTTGTGCAGCTCCCTTCCAAATACACTTGGACTTGAAGTGAAG 579
 Db 480 GACCCCTTCATGTTCTTCTGTGCAGTTCCCCCAACATGCACACCCAGACATGAATATTAAG 539
 Oy 580 AGTCTTGTGCTGGGTCCATTAATACCA--CTTCACCTTGGCTTACTGACTGCTG 637
 Db 540 AGTCTTGTGCTGAAGACCATATGACACCAAACTCCACCTTGACAAAGTCAGTACGTGG 599
 Oy 638 GAGGTGATATCCAGTGGGTGGGATCAACATCCCTTAAGGGCTGAAGCTCAAGCTGCTGC 697
 Db 600 CAGGTAAATCCAGTGGGTGGTACCAAGCTTCTCTGGACCTGMACTAAGCTAAGCTG--TTGC 658
 Oy 698 AGCAGAGGGACACTGCACCTGAGAGTGTACTTGAAGGGCCAGGTAGCCAGAGCTCAAGTC 757
 Db 659 AGCCAGGTACACTTACTGTGAGAGTGTGATACCAAGAAAGCAGAGTGGCCACAGTGTCTTG 718
 Oy 758 ATCTGTGGGTGAGACTGCCCCATAGGCTTTTGTGTGACAGCCCGGTGTGAGATTTGGGGCA 817
 Db 719 ATCTGTGGGTGCTGTTCACAGAGCCCTTTGTGTGACAGCCC-AGTAAAGGTGAGGGCAAC 777
 Oy 818 CACCAAGAT 825
 Db 778 CTCGCGGTT 785

RESULT	7
B1145698	
LOCUS	841 bp mRNA linear EST_05-JUL-2001
DEFINITION	602909844F1 NCI_CGAP_L19 Mus musculus CDNA clone IMAGE:5050810 5' , mRNA sequence.

ACCESSION	BI145698	GI:1460569
VERSION	BI145698.1	
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.ncl.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
1 (bases 1 to 841)

Email: cgabds-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LUNL)

Plate: LLAM1138 row: h column: 11
High quality sequence stop: 835.

FEATURES	Location/Qualifiers
Source	1, .841

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/strain="FVB/N"
/db_xref="taxon:10090"
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/clone_id="NCI_CGAP_L19"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: 11ver; Vector: PCMV-SPORT6; Site: 1; NCI;
Site: 2; Salt: Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT
181 a 238 c 221 g 201 t

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Query Match	17.6%	Score 399;	DB 10;	Length 841;
Best Local Similarity	84.3%	Pred. No. 1.6e-52;		
Matches 461; Conservative	0;	Mismatches 85;	Indels 1;	Gaps 1

OY	675	GGCTGAACTCAACTACCTCCCTGACACCGGCGACCTGACCTGGACTGACTGAAC	734
		1	
Db	1	GACCTGAACCTCAACCTCTCTTGACACCA - GGACACCTTACTCTGGACTGGTACACGAA	59
OY	735	GCCAGGTAGCCAGAGCTCAGTCATCCCTGGGTGGAGGGCCCAATAGGCCCTTTTGTGGCAG	794
Db	60	GCCAGGTGGCCCAAGTTCTTGATCTCTGGGCTGGTTTCCCAAGAGCCTTTTGTGGCAG	119
OY	795	CCCCGGTGAAGTGTGGGGCAACACAGATTCAACGACGAGGAGTGCACAAAGAG	854
		1	
Db	120	CCCAAGTAAAGGTTGAGGGCAAGCATCGGGTCCGCGGACAGTATCGATTCCACAGGGG	179
OY	855	GGTTCAGAGTGGCTTCGACAACAAGTTTTCGTGCACTTCCTGAGATTGGCTGCACG	914
Db	180	CGTCCAGATGTGGCTTCGACAACAAGTTCTTGAGACTTCCTGTGAGATTGGCTGGAATG	239
OY	915	ACTGATCATCCAGCCTGAGGGGTACCGCATGAACTTCGATAGGGCAATGGCCCACTAC	974
Db	240	ACTGATCATCCAGCCTGAGGGGTACCGCATGAACTTCGACCGGCAATGGCCCACTAC	299
OY	975	ACATAGCAGGCATCCCTGGTATTTGCTGCCCTTTCACACTGCAGTGCATCTCTCA	103
		1	
Db	300	ATGTGGCAGGCATCCCTGGTATTTGCTGCCCTTTCACACTGCAGTGCATCTCTCA	359
OY	1035	AGGCCAACACGCTGCGAGGGACCACTGGAGGGGGCTCATGCTGTGTAACCCACCGCCGGC	109
		1	
Db	360	AAGCCAAACGACTGCTGGGACCACTGGAGGGGGCTCATGCTGTGTAACCCACCGCCGGC	419
OY	1095	GCCCCCTGTCTCTGCTTATTATGACAGGACAGCAACATTGTCAAGACTGACATPACCTG	115
		1	
Db	420	GCCCTGTGTCTCTCTTACTATGACAGGACGCAACATTGTCAAGAGCGGATPACCTG	479
OY	1155	ACATGTGATGAGGCGCTGTGGGTGACATTATCTATGTGTGGTATGAGCCACCCCAAGT	121
		1	
Db	480	ACATGTGTGTGAGGCGCTCGGGGTGATTAGCTTATGGGTATPACAGGCTCCCTGAGGT	539
OY	1215	TGCATGG 1221	
		1	
Db	540	AGAATGG 546	

RESULT	8
BII48079	
LOCUS	BII48079
DEFINITION	602912428P1 NCI- <i>CGAP-L19</i> Mus musculus CDNA clone IMAGE:505347L.5'
ACCESSION	BII48079
VERSION	BII48079.1 GI:14608080

Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>

Plate: L1AM11145 row: 9 column: 08
High quality sequence stop: 887.

FEATURES	Location/Qualifiers
source	1. .941

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/organism="Mus musculus"
/strain="FVB/N"
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/clone_id="NCI-CGAP-L19"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pcMV-SPORT6; site_1: NCI;
site_2: SalI; cloned unidirectionally. Primer: Oligo dT
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI-CGAP library."

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Query Match	17.48;	Score 396;	DB 10;	Length 941;
Best Local Similarity	83.98;	Pred. No. 4.3e-52;		
Matches 483; Conservative	0;	Mismatches 90;	Indels 3;	Gaps 3;

Qy	647	GCACGTGGCTGSCATCAACTCCCCCTTAGG - GCGTAAGCTCAAGCTGCCGACGCAGAG	705
Db	1	GCACAGGGCTGGTACACAGCTTCTCTGGGAACCTGAAGGCTCAAGGCTGTTTGGACGCAGAGA	60
Qy	706	GCACCTGACCCCTGGAGCTGGTACTTTGAAGGCGCAGTAAAGCCAGAGCTCAGTATCTCTGGG	765
Db	61	-CACCTTACTCTGGAGCTGGTACTTACCAAGAAAGCAGGTGGCCCAAGTTCCTTATCTCTGGG	119
Qy	766	TGGAGCTGCCCATAGGCCCTTTTGTGGCAGGCCCGGTGAGAGTTTGGGGGCAACACCAAT	825
Db	120	CTGGTTTTTCCCAAGGCCCTTTTGTGGCAGCCCAAGTAAGGTTGAAGGCGAACACATCGGCT	179
Qy	826	TTCACGAGACGAGGCATTCAGCTGCCCAAGAGAGGCTCCAGAGTGTGCTTCGACAGAGATTCTT	885
Db	180	TGCGCCGGGAGAGTATCGATTGCC - AGGGGGGTCCAGAGATGTCTCTCCACAAGAGTTCTT	238
Qy	886	TGTGACATTCCGTGAGATTGGCTTGCGACGACTGGATCATCCAGCCGTGAAGGGCTAGGCCAT	945
Db	239	CGTACACTTCCGTGAGATTGGCTGGAATAGCTGATCATCCAGCCTGAAGGCTTATGCCAT	298
Qy	946	GAACCTTTCGATAGGGCAGTGGCCCACTTACACATAGCAGGCAATGCCGTATTGTGTCCTC	1005
Db	299	GAACCTTTCGACCGGGCAGTGGCCCACTTACATGTGGCAGCAATCCTTGCATCTCTGCTC	358
Qy	1006	CTTTCACACTCAGTGTCTCAATCTTTCGAAAGGCGAAACAGCTGAGAGCACCATGTGAGG	1065
Db	359	CTTTCACACTCAGTGTCTCAATCTTTCGTAAGCAACAGCAGTGTGCGACCACTGTGGCAG	418
Qy	1066	GGGCTCATGTGTTGTATCCCAAGGCCCGGGGCCCTGTCTGCTCTATTATTCACAGAGA	1125
Db	419	GGGCTCTGGCTGGCTGCTTACATCTCGGGCCCTGTGCTTTTGGCTTACATATGACAGGA	478
Qy	1126	CAGGACATTTGTAAACATGCATTAATCTTACATGGTAACTAGAGGCTTGTGGGTGCAGTTA	1185

Db 479 CAGCAACATTTTCAGACGATATACCTGACAGTGGTCGAGGCGGCGGTAGTTA 538
 Oy 1186 GTCTATGTGTGTATGGGACCCCAAGGTTGCATGG 1221
 Db 539 GCTTATGGGTATACAGGCTGCTGAGGTAGTAATGG 574

RESULT 9
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 DEFINITION mRNA sequence.
 ACCESSION BF232704 GI:11142342
 VERSION BF232704.1 GI:11142342
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 816)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM9435 row: 9 column: 23
 High quality sequence stop: 714.
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 /db_xref="taxon:10090"
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 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: liver; Vector: pCMV-Sport6; Site_1: NciI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.9 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP library."
 BASE COUNT 167 a 253 c 221 g 175 t

Query Match 16.6%; Score 378; DB 10; Length 816;
 Best Local Similarity 74.5%; Pred. No. 2,8e-49;
 Matches 556; Conservative 0; Mismatches 180; Indels 10; Gaps 6;

Oy 29 TTCTTCAGAGGCTCTGCGACGACGAGAGTTGAGACCACTGTTGAGACCTTGA 88
 Db 7 TTCTTCAGAGGCTCTGCGACGACGAGAGTTGAGACCACTGTTGAGACCTTGA 66
 Oy 89 CCCTGAGTCTGTATGCTCAAGAGGCGCTTCCCGCAATGACCTCCCTGATTTGCTG 148
 Db 67 TATAGGCT-TGGGTCTTTAAGAGGCTATCTCCAGCAATGCGCTCTGCTGCTG 125
 Oy 149 GCTTTTCTCTGCTGCTGCTCAACACAGATGCGCACTCCAGAGCTGGCGTCACTGCA 208
 Db 126 GCTCTTCTGTTCTGACTGCAACACAGATGCACTCCAGAGCTGGCGTCACTGCA 185
 Oy 209 GCATGTGGGGGGCCACCTTGAATGAGAGAGCCAGCGGAGCTGCTTTTATATCGGC 268
 Db 186 GCATGTGGGGGGCCACCTTGAATGAGAGAGCCAGCGGAGCTGCTTTTATATCGGC 245
 Oy 269 AAGGAGGAGCTTGTGACAGGAGCTGACCTGACCGGCGCAACTGAACGCGCTGTG 328
 Db 246 AAGGAGGAGCTTGTGACAGGAGCTGACCTGACCGGCGCGCAACTGACGCGCTGTG 305

Oy 329 TCAGAGCTGCTTTGAGGAGTGTACCTGACACCTCCAGCGGGCTCCACAGAGGGGCACTT 388
 Db 306 TCAGAGAGGGGCTCTCAGAGACCGCGCTGACGGCGCTGAGCGGGAACCTTG 365
 Oy 389 CTAGAG--GACACAGGGAACAGGAATGTGAATCATCTGCTTTGCTGAGACAGGCTTC 445
 Db 366 TTGAGCATGACACAGAGACAAAGAAATATGAGATCATCATCTTCTGTCAGACAGCTTC 425
 Oy 446 TCCACATCAACACAGACGCTGCTGATTTTCACTTCCTGATAGAACTGCTGGTGAC 505
 Db 426 TCCACATCAACACAGACCGCGCTGAGTTCACCTT---CTCTGATGAATGCGCACTGGC 482
 Oy 506 AGCAGAGTCCACAGAGCGGACGCTCATGTTCTTTGTCAGAGCTCCCTTCAATACCACTTGG 565
 Db 483 ATGAGAGTCCGCGACACCGCGCTCATGTTCTGTCGACAGTTCCCGCCCAATGCGCACAG 542
 Oy 566 ACCTTGAAGTACAGAGTCTTGTGCTGGGTCAACATATACCAACTCAGCTTGGCTACT 625
 Db 543 ACCATGAATATATAGAGTCTTGTGCTAAGACCATATGACACCAAACTCAGCTTGGACAGT 602
 Oy 626 CAGTACCTGCTGAGGTGATGCGAGTGGCTGATCACTCCCTTACGAGCTTGAAGCGCTGAAGC- 684
 Db 603 CAGTACCTGCTGAGGTGATGCGAGTGGCTGATCACTCCCTTACGAGCTTGAAGCGCTGAAGC- 662
 Oy 685 TCAGAGTGGCTGCA-GCCAGGGGACCTGAC-CCTGAGCTGTGACTTGAAGCGGAGCTA 742
 Db 663 TCAGAGTGGCTGCA-GCCAGGGGACCTGAC-CCTGAGCTGTGACTTGAAGCGGAGCTA 722
 Oy 743 GCCCAGAGCTCAGTATCTGCTGGGTGG 768
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RESULT 10
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 DEFINITION mRNA sequence.
 ACCESSION BF533968
 VERSION BF533968.1 GI:11621331
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 975)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM9782 row: 1 column: 08
 High quality sequence stop: 659.
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 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: liver; Vector: pCMV-Sport6; Site_1: NciI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.9 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP library."
 BASE COUNT 190 a 297 c 266 g 222 t

GenCore version 5.1.3
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OM protein - protein search, using sw model

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Run on:      October 11, 2002, 22:15:33 ; Search time 41 Seconds
              (without alignments)
              953,609 Million cell updates/sec
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Title: US-09-684-383-2
 Date of report: 1949

Partial score: 1045
Sequence: 1 MTSSLLAEFLAFTTVATP.....DSNIVKTDIPDMVEACGCS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	1849	100.0	352	17	AA89729	Transforming growth factor- β
2	1838	99.4	352	22	AA870530	Human TGF- β 1
3	1392	75.3	352	19	AA870530	Human TGF- β 1
4	664	35.9	350	17	AA870530	Human TGF- β 1
5	664	35.9	350	17	AA870530	Human TGF- β 1
6	655	35.4	350	19	AA870530	Human TGF- β 1
7	648	35.0	350	19	AA870530	Human TGF- β 1
8	598.5	32.4	407	21	AA870530	Human TGF- β 1
9	598.5	32.4	407	21	AA870530	Human TGF- β 1
10	590	31.9	355	8	AA870530	Human TGF- β 1
11	578	31.3	351	8	AA870530	Human TGF- β 1

12	558.5	30.2	427	8	AAPI0200
13	557	30.1	426	8	AAPI0203
14	557	30.1	426	21	AAV92016
15	557	30.1	426	21	AAV92018
16	555	30.0	426	11	AAAR05413
17	469	25.4	87	14	AAAR54447
18	444	24.0	127	12	AAAR10991
19	439.5	22.8	303	22	AAAO02968
20	422	22.8	288	7	AAPE6518
21	388.5	21.0	121	22	AAAB73203
22	375	20.3	122	22	AAAB73202
23	373	20.2	130	7	AAPE60520
24	369.5	20.0	115	13	AAAR26482
25	368.5	19.9	115	13	AAAR25129
26	368.5	19.9	115	14	AAAR31623
27	368.5	19.9	116	13	AAAR25127
28	366.5	19.8	115	8	AAAP71197
29	366.5	19.8	115	8	AAAP71177
30	366.5	19.8	115	11	AAAR08216
31	361.5	19.6	115	9	AAAP80020
32	360	19.5	116	13	AAAR26481
33	358	19.4	116	11	AAAR05444
34	357	19.3	116	8	AAAP71196
35	357	19.3	116	8	AAAP71176
36	357	19.3	116	9	AAAP80019
37	357	19.3	116	9	AAAP80261
38	357	19.3	116	11	AAAR05445
39	357	19.3	116	11	AAAR08213
40	357	19.3	116	13	AAAR25128
41	357	19.3	116	14	AAAR31622
42	357	19.3	116	21	AAAY67949
43	354	19.1	130	12	AAAR12088
44	352	19.1	130	12	AAAR10990
45	345	18.7	116	9	AAAP81306

ALIGNMENTS

RESULT	1
ID	AAR89729 standard; Protein: 352 AA.
AC	AAR89729;
DT	09-AUG-1996 (first entry)
DE	Transforming growth factor beta MP-121.
KW	TGF-beta; MP-121; mitogen; differentiation; induction; promotion;
KW	maintenance; morphogen; tissue regeneration; dental implantation;
KW	wound healing.
OS	Homo sapiens.
FH	Key Location/Qualifiers
FT	Protein 237..352
FT	/label= mature_protein
PN	DEJ9511243-A1.
PD	04-JAN-1996.
PF	27-MAR-1995; 95DE-1011243.
PR	01-JUL-1994; 94DE-1423190.
PA	(BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
PI	Bechtold R, Neidhardt H, Pohl J, Hoetten G;
XX	WPL: 1996-050788/06.
DR	N-PDSB; AAT11104.

XX DNA encoding transforming growth factor beta MP-121 - has mitogenic
 PT and differentiation-inducing activity, e.g. for use in wound healing
 XX
 PS Claim 7; Page 11; 15pp; German.

CC A cDNA library prepared using total RNA from human liver was
 CC subjected to PCR amplification using primers corresp. to conserved
 CC regions within the TGF-beta family. Amplification products were
 CC subcloned and sequenced: one clone (designated PSK-MP121) was found
 CC to contain a new sequence. Part of the insert from the clone was
 CC used to re-screen the human liver cDNA library and a 2272 bp fragment
 CC coding for a TGF-beta-like protein (i.e. the present sequence) was
 CC isolated. This protein has mitogenic and differentiation-inducing
 CC properties making it (or fusion proteins comprising it or heterodimers
 CC of the protein with a cysteine knot motif protein) useful for inducing
 CC tissue regeneration, e.g. for wound healing, inducing growth of
 CC hepatic tissue or bone marrow precursor cells, treating fertility
 CC disorders, etc.
 XX

XX Sequence 352 AA:

Query Match 100.0%; Score 1849; DB 17; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.1e-171;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSSLLAFLLAFTTATPRAGGCGPGLLESGRELLDLAKRSILDKLHTQR 60
 DB 1 MTSSLLAFLLAFTTATPRAGGCGPGLLESGRELLDLAKRSILDKLHTQR 60
 QY 61 PTLNRPVSRAALRTALQHLHGVPOGALLDNRECEIIISFAETGLSTINOTRIADPHFS 120
 DB 61 PTLNRPVSRAALRTALQHLHGVPOGALLDNRECEIIISFAETGLSTINOTRIADPHFS 120
 QY 121 DRTAGDREVQOASLMFFVQLPSNTTTLKRVLYLGPHTNLTATQYLLEVDASGMHQL 180
 DB 121 DRTAGDREVQOASLMFFVQLPSNTTTLKRVLYLGPHTNLTATQYLLEVDASGMHQL 180
 QY 181 PLGPEAQAACSGCHLTLELVLEGVOAOSVILGGAHRPFAARVVGKQIHRRGIDC 240
 DB 181 PLGPEAQAACSGCHLTLELVLEGVOAOSVILGGAHRPFAARVVGKQIHRRGIDC 240
 QY 241 OGGSRMCCROEFFVDFREIGWDMIIOPEGYAMNFCIGCPLHAGMGIAASHFTAVLN 300
 DB 241 OGGSRMCCROEFFVDFREIGWDMIIOPEGYAMNFCIGCPLHAGMGIAASHFTAVLN 300
 QY 301 LKANTAAAGTTGGSCCVTARPPISLLYDRDSNIVKTDIPDNVEACGCS 352
 DB 301 LKANTAAAGTTGGSCCVTARPPISLLYDRDSNIVKTDIPDNVEACGCS 352

RESULT 2
 AAB70530
 ID AAB70530 standard; Protein: 352 AA.

XX AAB70530:

XX 08-MAY-2001 (first entry)

XX Human TGF-beta MP121 protein sequence SEQ ID NO:4.

XX KW Human: transforming growth factor-beta; monomeric protein; MP52;
 KW MP121; dimeric protein; TGF-beta; vulnary; antitumor; neutrotropic;
 KW neuropeptide; antifertility; osteopathic; gene therapy; bone;
 KW cartilage; dental; wound healing; connective tissue.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT Misc-difference 316 /note= "unspecified"

XX EPI074620-A1.

XX 07-FEB-2001.

XX 06-AUG-1999; 99EP-0115613.

XX 06-AUG-1999; 99EP-0115613.

XX (HYGE-) HYGENE AG C/O MAEDER & BAUMGARTNER TREGH.

XX NPI: 2001-228100/24.

XX N-PSDB: AAF74421.

PT Novel monomeric protein of transforming growth factor-beta family for
 PT prevention or therapy of diseases associated with bone, cartilage
 PT damage, promotion of wound healing, has substitution or deletion of
 PT cysteine

PS Claim 10; Page 21-22; 31pp; English.

CC The present invention describes a protein (I) selected from the members
 CC of the transforming growth factor-beta (TGF-beta) superfamily, which is
 CC monomeric due to substitution or deletion of a cysteine which is
 CC responsible for dimer formation. Also described are: (1) nucleic acid
 CC (II) encoding (1); (2) expression vector (III) containing (II) in a
 CC suitable vector system; (3) host cell (IV) containing (III) capable of
 CC producing (I); and (4) a pharmaceutical composition (V) containing (I),
 CC (II), (III) or (IV). (I) has vulnary, antitumor, neutrotropic,
 CC neuroprotective, antifertility and osteopathic activities, and can be
 CC used in gene therapy. (V) is useful for the prevention or therapy of
 CC diseases for which also the dimeric form of the protein would be
 CC indicated. Diseases treatable include diseases associated with bone
 CC and/or cartilage damage or affecting bone and/or cartilage disease or
 CC situations in which cartilage and/or bone growth is desirable, for spinal
 CC fusion, for damaged or diseased tissue associated with connective tissue
 CC including tendon and/or ligament, peridontal or dental tissue including
 CC dental implants, neural tissue including CNS tissue and neuropathological
 CC situations, tissue of the sensory system, liver, pancreas, cardiac,
 CC blood vessel, renal, uterine and thyroid tissue, skin, mucous membrane,
 CC endothelium, epithelium, for promotion or induction of nerve growth,
 CC tissue regeneration, angiogenesis, wound healing including ulcers, burns,
 CC injuries or skin grafts, induction of proliferation of progenitor cells
 CC or bone marrow cells, for maintenance of a state of proliferation or
 CC differentiation, for treatment or preservation of tissue or cells for
 CC organ or tissue transplantation, for integrity of gastrointestinal lining
 CC and for treatment of disturbances in fertility, contraception or
 CC pregnancy. The present sequence represents the specifically claimed
 CC TGF-beta monomeric protein MP121, from the present invention.

XX Sequence 352 AA:

Query Match 99.4%; Score 1838; DB 22; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.6e-170;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSSLLAFLLAFTTATPRAGGCGPGLLESGRELLDLAKRSILDKLHTQR 60
 DB 1 MTSSLLAFLLAFTTATPRAGGCGPGLLESGRELLDLAKRSILDKLHTQR 60
 QY 61 PTLNRPVSRAALRTALQHLHGVPOGALLDNRECEIIISFAETGLSTINOTRIADPHFS 120
 DB 61 PTLNRPVSRAALRTALQHLHGVPOGALLDNRECEIIISFAETGLSTINOTRIADPHFS 120
 QY 121 DRTAGDREVQOASLMFFVQLPSNTTTLKRVLYLGPHTNLTATQYLLEVDASGMHQL 180
 DB 121 DRTAGDREVQOASLMFFVQLPSNTTTLKRVLYLGPHTNLTATQYLLEVDASGMHQL 180
 QY 181 PLGPEAQAACSGCHLTLELVLEGVOAOSVILGGAHRPFAARVVGKQIHRRGIDC 240
 DB 181 PLGPEAQAACSGCHLTLELVLEGVOAOSVILGGAHRPFAARVVGKQIHRRGIDC 240
 QY 241 OGGSRMCCROEFFVDFREIGWDMIIOPEGYAMNFCIGCPLHAGMGIAASHFTAVLN 300
 DB 241 OGGSRMCCROEFFVDFREIGWDMIIOPEGYAMNFCIGCPLHAGMGIAASHFTAVLN 300

QY 301 LKANTAGCTGGCGCCVPTARRPLSLLYDRDSNVKTDIPDMVVEACGCS 352
 |||||
 Db 301 LKANTAACTGGGSCVPTARRPLSLLYDRDSNVKTDIPDMVVEACGCS 352

RESULT 3
 AAM60617 standard: Protein: 352 AA.
 ID AAM60617
 AC AAM60617:
 XX
 DT 01-FEB-1999 (first entry)
 XX
 DE Murine liver activin beta c polypeptide.
 XX
 KW Liver activin: beta c; beta e; cell differentiation; haematopoiesis;
 KW erythroid; ovarian follicular maturation; hormone; neuronal survival;
 KW spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;
 KW osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunosassay;
 KW menstrual disorder; transgenic; modulator.
 XX
 OS Mus sp.
 XX
 FH Key
 FH Peptide
 FT Location/Qualifiers
 FT 1..20
 FT /note="signal sequence"
 FT 11..113
 FT /note="Asn is putatively N-glycosylated"
 FT 143..145
 FT /note="Asn is putatively N-glycosylated"
 FT 161..163
 FT /note="Asn is putatively N-glycosylated"
 FT 173..175
 FT /note="Asn is putatively N-glycosylated"
 FT 21..236
 FT /note="propeptide domain"
 FT 230..236
 FT /note="endoproteolytic cleavage site"
 FT 237..352
 FT /note="mature growth factor domain"
 FT Domain
 PN MO9822492-A1.
 XX
 PD 28-MAY-1998.
 XX
 PF 20-NOV-1997: 97WO-US20862.
 XX
 PR 20-NOV-1996: 96US-0752919.
 XX
 PA (UNMI) UNIT MICHIGAN.
 XX
 PI Bonadio J, Fang J;
 XX
 DR WPI: 1998-312408/27.
 DR N-PSDB: AAV38237.
 XX
 PT New isolated nucleic acid encoding sub-units of liver activin
 PT useful for regulating growth and differentiation of cells, e.g. for
 PT treating liver, bone and haematopoietic disorders
 XX
 PS Claim 16: Fig 1: 141pp: English.
 XX

This represents a murine liver activin beta c polypeptide. Sequences
 derived from beta c cDNA clone is used for screening and cloning a liver
 activin beta e gene. Disorders of cell growth or differentiation (or
 susceptibility to them) are diagnosed by measuring liver activin gene
 activity or by detecting a mutation in the liver activin gene. Disorders
 of haematopoiesis, erythroid differentiation, ovarian follicular
 maturation, hormone secretion, neuronal survival, spermatogenesis, bone
 formation, insulin secretion or cardiac morphogenesis are some conditions
 that can be diagnosed using the liver activin. Cell growth and
 differentiation can be stimulated by treatment with an liver activin

CC compound or agent that upregulates the compound's expression. Antagonists
 CC can be used to treat liver diseases while agonists can be used to
 CC increase growth and regeneration of liver tissue. The liver activin
 CC compound may also induce bone growth (e.g. for treating osteoporosis or
 CC osteomalacia) or haematopoiesis, particularly erythropoiesis, e.g. for
 CC treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies
 CC are useful in immunosassays, to generate anti-idiotypic antibodies (which
 CC bind to liver activin receptors) and to inhibit liver activin. Also,
 CC transgenic animals containing liver activin gene can be used to produce
 CC the liver activin (in correctly processed and modified forms) proteins,
 CC or the transgenic animals, are useful for screening for liver activin
 CC modulators.
 CC
 CC
 SQ Sequence 352 AA:

Query Match 75.3%; Score 1392; DB 19: Length 352;
 Best Local Similarity 75.9%; Pred No. 8.5e-127;
 Matches 268; Conservative 32; Mismatches 51; Indels 2; Gaps 2;

QY 1 MTSLLAFLLAPTTVAPPRAGGCPACGGPTLEESORELLDLAKRSILDKLHLTOR 60
 |||||
 Db 1 MASSLLALLFLPPTTVVANKTEGPCPCAGAIFFLESORELLDLAKRSILDKLHLTOR 60

QY 61 PTLNRPVSRALRTALQHLGVQGALLF-DNREOCETISFAETGLSTINTRLDPHFS 119
 |||||
 Db 61 PILSRPVSRAKLTALQRLGRPRRETLLEHDORQREYEILSPADLDLSTINOTRLEPHFS 120

QY 120 SDRAGDREVOQASLMPFVLPSPNTTTLKRVRLVGLPHTNTLTATQYLLVDASGMHQ 179
 |||||
 Db 121 G-RNASGHEVRQTFMFVFPFHNAOTMIRVLRLPYDNTLTLSQVVOVNASGMWQ 179

QY 180 LPLGPEAOACSGCHLTLELVESQVASSVYIGAAHRRPFAARVGGKQIHRRGID 239
 |||||
 Db 180 LLLGPEAOACSGCHLTLELVESQVASSVYIGAAHRRPFAARVGGKQIHRRGID 239

QY 240 CCGSRMCCROEFVDFREIGMDHMTIIOPEGYAMNFCGCPHIGMGIAASFHTAVL 299
 |||||
 Db 240 CCGSRMCCROEFVDFREIGMDHMTIIOPEGYAMNFCGCPHIGMGIAASFHTAVL 299

QY 300 NLKNTAGCTGGGSCVPTARRPLSLLYDRDSNVKTDIPDMVVEACGCS 352
 |||||
 Db 300 NLKNTAAAGCTGGGSCVPTARRPLSLLYDRDSNVKTDIPDMVVEACGCS 352

RESULT 4
 AAR92754
 ID AAR92754 standard: Protein: 350 AA.
 XX
 AC AAR92754:
 XX
 DT 21-JUL-1996 (first entry)
 XX
 DE Human growth differentiation factor-12.
 XX
 KW Growth differentiation factor-12; GDF-12; liver; cell proliferation;
 KW cancer; diagnosis; therapy; transforming growth factor beta.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH Modified-site
 FT Location/Qualifiers
 FT /label="N-glycosylation_site
 FT Cleavage-site
 FT 232..236
 FT 237..350
 FT Region
 FT /label="C-terminal_region
 FT /note="GFR-12 active C-terminal fragment"
 XX
 PN MO9602559-A1.
 XX
 PD 01-FEB-1996.
 PD 12-JUL-1995: 95WO-US08745.
 XX

PR 26-SEP-1994: 94US-0311370.
 PR 13-JUL-1994: 94US-0274215.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.
 PA
 PI Esquelea AF, Lee S;
 XX
 XX WPI: 1996-105850/11.
 DR N-PSDB: AAT16883.
 XX
 PT DNA encoding Growth Differentiation Factor-12 - used in diagnostic
 PT and therapeutic methods esp. in methods for treating a cell
 PT proliferative disorder of liver origin
 XX
 PS Claim 3: Page 40-43: 52pp: English.

CC Human growth differentiation factor-12 (GDF-12 - AAR92754) is a new
 CC member of the transforming growth factor beta superfamily that is
 CC expressed specifically in liver. It can be obt'd. by expression
 CC of a cDNA clone (AAT16883) derived from adult liver in transformed
 CC host cells. GDF-12 possesses activities that will make it useful
 CC in the treatment of liver disorders, e.g. disease states in which
 CC liver function is compromised, or cellular proliferative disorders
 CC such as hepatocellular carcinoma. In can also be used to expand
 CC liver cells in culture and to raise diagnostic antibodies.

SO Sequence 350 AA:

Query Match 35.9%; Score 664; DB 17; Length 350;
 Best Local Similarity 43.3%; Pred. No. 5, 1e-56;
 Matches 156; Conservative 52; Mismatches 118; Indels 34; Gaps 14;

OY 9 FLTLAPTTVATPRAGGCGPAGGPTLESGRELLDLAKRSLDKLHLPRTLRPVG 68
 DB 9 WLVLMLALVRAOGTGVPCSGSGSKLAPQERALVLELAKQQLDGLHLSRRIHP 68
 OY 69 RAALRTALOHVHVGOGALLDNRQECETISFAE-TGLSTINOTRLDPHFSSDRTAGDR 127
 DB 69 QALITRALRLQ---PESVAPNGE---EVISFATVDTSTAYSLSLTLSTPRS---H 119
 OY 128 EVOQASLMFVQLPSNTWTWTKVRLVLP---HNTNLTATQVLEVDASGMHQLPLG 183
 DB 120 HLYHARLMLHV-LPT-LPTGLCRIFRMGPRRRRSGSLTLEAHHTNL---GMHTLTLP 174
 OY 184 PEAQACSGCHLTLEL---VLEGO---VAQSSVILGGAH-RPFVAVRVG--GKHQIH 234
 DB 175 SSGLRGKSGVTLKQLDLCRPLEGNSVTGQPRRLDPTAGHOQFLELKRANEPGAGRAR 234
 OY 235 RRGIDCGGSRMCCROEFVDFREIGMHWIIOPEGYAMNFCIGCPRHIAAGPIAASF 294
 DB 235 RRTPTCEPATPLCCRDHIVDFQELGMRDWIIOPEGYOLNYSGGCPRHLAGSGIAASF 294
 OY 295 HTAVLNLKANT--AAGTTGGSCCVPTARRPLSLLYDRDSNIYKTDIPDMVVEACGS 352
 DB 295 HSAVFSLLKANNPWPAST---SCCVPTARRPLSLLYLDHNGNVKTDVPMVVEACGS 350

RESULT 5

AAM93672
 ID AAM93672 standard; Protein: 350 AA.

AC AAM93672;

DT 06-NOV-2001 (first entry)

DE Human polypeptide, SEQ ID NO: 3558.

OS Human; full length cDNA; cDNA synthesis; oligo-capping.

XX Homo sapiens.

XX EPI130094-A2.

XX

PD 05-SEP-2001.

XX 07-JUL-2000; 2000EP-0114089.

XX 08-JUL-1999; 99JP-0194486.

PR 11-JAN-2000; 2000JP-0118774.

PR 02-MAY-2000; 2000JP-0183765.

XX (HELI-) HELIX RES INST.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

XX Wakematsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WPI: 2001-524255/58.

DR N-PSDB: AAK94607.

XX 830 Primers useful for synthesizing full length cDNA clones and their

XX use in genetic manipulation -

PS Claim 8: SEQ ID NO 3558: 1380bp + sequence listing; English.

XX The invention relates to primers for synthesizing full length cDNA

XX clones. 830 cDNA molecules encoding a human protein have been

XX isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA

XX molecules have been determined. Primers for synthesizing the full length

XX cDNA are useful for clarifying the function of the protein encoded by

XX the cDNA. The full length clones were obtained by construction of full

XX length enriched cDNA libraries that were synthesised by the oligo-capping

XX method. The primers enable the production of the full length cDNA easily

XX without any special methods. The present sequence is a polypeptide

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in CD-ROM format directly from EPO.

SO Sequence 350 AA:

Query Match 35.9%; Score 664; DB 22; Length 350;
 Best Local Similarity 43.3%; Pred. No. 5, 1e-56;
 Matches 156; Conservative 52; Mismatches 118; Indels 34; Gaps 14;

OY 9 FLTLAPTTVATPRAGGCGPAGGPTLESGRELLDLAKRSLDKLHLPRTLRPVG 68
 DB 9 WLVLMLALVRAOGTGVPCSGSGSKLAPQERALVLELAKQQLDGLHLSRRIHP 68
 OY 69 RAALRTALOHVHVGOGALLDNRQECETISFAE-TGLSTINOTRLDPHFSSDRTAGDR 127
 DB 69 QALITRALRLQ---PESVAPNGE---EVISFATVDTSTAYSLSLTLSTPRS---H 119
 OY 128 EVOQASLMFVQLPSNTWTWTKVRLVLP---HNTNLTATQVLEVDASGMHQLPLG 183
 DB 120 HLYHARLMLHV-LPT-LPTGLCRIFRMGPRRRRSGSLTLEAHHTNL---GMHTLTLP 174
 OY 184 PEAQACSGCHLTLEL---VLEGO---VAQSSVILGGAH-RPFVAVRVG--GKHQIH 234
 DB 175 SSGLRGKSGVTLKQLDLCRPLEGNSVTGQPRRLDPTAGHOQFLELKRANEPGAGRAR 234
 OY 235 RRGIDCGGSRMCCROEFVDFREIGMHWIIOPEGYAMNFCIGCPRHIAAGPIAASF 294
 DB 235 RRTPTCEPATPLCCRDHIVDFQELGMRDWIIOPEGYOLNYSGGCPRHLAGSGIAASF 294
 OY 295 HTAVLNLKANT--AAGTTGGSCCVPTARRPLSLLYDRDSNIYKTDIPDMVVEACGS 352
 DB 295 HSAVFSLLKANNPWPAST---SCCVPTARRPLSLLYLDHNGNVKTDVPMVVEACGS 350

RESULT 6

AAM60619
 ID AAM60619 standard; Protein: 350 AA.

AC AAM60619;

DT 01-FEB-1999 (first entry)

XX

DE Human liver activin beta e polypeptide.

KM Liver activin: beta c; beta e; cell differentiation; haematopoiesis;
 KM erythroid; ovarian follicular maturation; hormone; neuronal survival;
 KM osteomalacia; bone; insulin; cardiac morphogenesis; osteoporosis;
 KM osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunoassay;
 KM menstrual disorder; transgenic; modulator; human.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FT Peptide 1..17

FT /note= "signal sequence"

FT Domain 18..236

FT /note= "propeptide domain"

FT Modified-site 198..200

FT /note= "Asn is putatively N-glycosylated"

FT Cleavage-site 232..236

FT /note= "endoproteolytic cleavage site"

FT Domain 237..350

FT /note= "mature growth factor domain"

FT

PN WO9822492-A1.

XX 28-MAY-1998.

PD 20-NOV-1997: 97WO-US20882.

XX

PF 20-NOV-1997: 96US-0752919.

XX

PR 20-NOV-1996: 96US-0752919.

XX

XX (UNMI) UNIV MICHIGAN.

PI Bonadio J, Fang J;

XX MPI: 1998-312408/27.

DR N-PSDB: AAV38240.

XX

PT New isolated nucleic acid encoding sub-units of liver activin -

PT useful for regulating growth and differentiation of cells, e.g. for

PT treating liver, bone and haematopoietic disorders

PT

PS Disclosure: Fig 5; 141pp: English.

XX

XX This represents a human liver activin beta e polypeptide. The invention

CC provides murine beta c and beta e polypeptides and the encoding genes.

CC Disorders of cell growth or differentiation (or susceptibility to them)

CC are diagnosed by measuring liver activin gene activity or by detecting a

CC mutation in the liver activin gene. Disorders of haematopoiesis,

CC erythroid differentiation, ovarian follicular maturation, hormone

CC secretion, neuronal survival, spermatogenesis, bone formation, insulin

CC secretion or cardiac morphogenesis are some conditions that can be

CC diagnosed using the liver activin. Cell growth and differentiation can be

CC stimulated by treatment with an liver activin compound or agent that

CC upregulates the compound's expression. Antagonists can be used to treat

CC liver diseases while agonists can be used to increase growth and

CC regeneration of liver tissue. The liver activin compound may also induce

CC bone growth (e.g. for treating osteoporosis or osteomalacia) or

CC haematopoiesis, particularly erythropoiesis, for treating haemophilia,

CC cystic fibrosis or menstrual disorders. Antibodies are useful in

CC immunoassays, to generate anti-idiotypic antibodies (which bind to liver

CC activin receptors) and to inhibit liver activin. Also, transgenic animals

CC containing liver activin gene can be used to produce the liver activin

CC (in correctly processed and modified forms) proteins, or the transgenic

CC animals, are useful for screening for liver activin modulators.

XX

XX Sequence 350 AA:

SQ

Query Match 35.4%; Score 655; DB 19; Length 350;

Best Local Similarity 42.8%; Pred. No. 3.9e-55;

Matches 154; Conservative 54; Mismatches 118; Indels 34; Gaps 14;

9 FLAAPTATVATPRAGCGCPACGPTLEUESORELLDLARSLIDKHLTORFTLRPPY 68

DB 9 WLVLMLALVRAQGTGVSCVSCGSKLAPQAERALVLELANQQLLEGHLTSRPRITHPP 68

OY 69 RAALPTALQHTHGVPQCALLEDNRECEIISFAE-TGLSTINQTRLDHFSSDRTAGDR 127

DB 69 QAAVTRALRRIQ---PGSVARGNE---EVSFATVYDSTRSAVSLSLTFILSTRS---H 119

OY 128 EVOQASLMEFFVQLPSNTTTLKRVNLVLP---HNNTLTLATQYLEVDASGMOLPLG 183

DB 120 HLYHARLMLVH-LPT-LGCTLCLETRFRMGPRRRRSGRSRTLLAEHITNL---CMHLLTLP 174

OY 184 PEAQACSGQGHITLEL---VLEGO---VAQSSVILGGAH-RPVRARVRVG---GRHDIH 234

DB 175 SSGLRGKSGVLTQLDLCRPLEGNSVTYGPRLDTPAGHQQPLELKITRANERAGARAR 234

OY 235 RRGIDCGGSRMCROEFFVDFREIGMHWITIOPEGYAMNFCIGCPDLITAGMGIASAF 294

DB 235 RRTPTCEPRTPLCCRRDHYVDFOELGMDWILDPBGVOLANCSGCPHLAGCGIASF 294

OY 295 HPAVNLKLANF--AAGTTGGSCCVPTARRPLSLIYDRDSNIVKTDIPDMVVEACGS 352

DB 295 HSAVFSLLKANNMPDAST----SCCVPTARRPLSLIYLDHNGNVKTDVDMVVEACGS 350

RESULT 7

AAW60618

ID AAW60618 standard; Protein: 350 AA.

XX

AC AAW60618;

XX

DT 01-FEB-1999 (first entry)

XX

XX Murine liver activin beta e polypeptide.

DE

XX Liver activin: beta c; beta e; cell differentiation; haematopoiesis;
 KM erythroid; ovarian follicular maturation; hormone; neuronal survival;
 KM spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;
 KM osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunoassay;
 KM menstrual disorder; transgenic; modulator.

XX

OS Mus sp.

XX

XX Key Location/Qualifiers

FT Peptide 1..21

FT /note= "signal sequence"

FT Domain 22..236

FT /note= "propeptide domain"

FT Modified-site 198..200

FT /note= "Asn is putatively N-glycosylated"

FT Cleavage-site 232..236

FT /note= "endoproteolytic cleavage site"

FT Domain 237..349

FT /note= "mature growth factor domain"

FT

PN WO9822492-A1.

XX 28-MAY-1998.

PD 20-NOV-1997: 97WO-US20882.

XX

PF 20-NOV-1997: 96US-0752919.

XX

PR 20-NOV-1996: 96US-0752919.

XX

XX (UNMI) UNIV MICHIGAN.

PI Bonadio J, Fang J;

XX MPI: 1998-312408/27.

DR N-PSDB: AAV38238.

XX

PT New isolated nucleic acid encoding sub-units of liver activin -

PT useful for regulating growth and differentiation of cells, e.g. for

PT treating liver, bone and haematopoietic disorders

PT

PS Claim 16; Fig 2; 141pp: English.


```

Db 85 RLOMRCRPNITHAVPKAAWVTALRLHA---GKVEDRGEVEIPLHLDGASPGADGQERVS 141
OY 97 EIISFAETGLSTINOTRLDFHSSDRTAGDRE--VQOASIMFVQLPSNTWTTL----- 148
PT 142 EIISFAETDGLASSRRLYEFLISNE--GNOLFFVQAALMLYLKL---LPVLEKGSRR 195
XX 149 KVRVLVL---GPHNTNLTATQYLLEVDASGWHQLPLRPEAQAACSGHLLTLEVLGQV 205
Db 196 KVRVAVVPEVDGEGHGRMNM-VEKRVDLKRSQWHTFPLTEAIOALEFERGERRLNLDVQCD 254
OY 206 AQSIVL-----GGAHREPVAAARVVG-GKHQIHRGIDCGGSRMCCROEFFVDFRE 258
XX 255 CQELAVVPEVDGEGHGRMNM-VEKRVDLKRSQWHTFPLTEAIOALEFERGERRLNLDVQCD 314
OY 259 IGHWDIITQPEGVAMNFCIGCCPLHAGMPGIAASFHTAVLNLKANPAAGTTGG--GSC 316
Db 315 IGHWDIITQPEGVAMNFCIGCCPLHAGMPGIAASFHTAVLNLKANPAAGTTGG--GSC 316
OY 317 CVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGCS 352
Db 372 CIPTKLSTMSMLYFDEYNIKRDVPMNIVEBCGA 407

RESULT 9
AAV92019
ID AAV92019 standard; Protein: 407 AA.
AC AAV92019;
DT 19-JUL-2000 (first entry)
XX Human activin B subunit.
XX human activin B subunit.
XX human activin B subunit; CKGF; mutant; cysteine knot growth factor;
XX hairpin loop; infertility.
XX Homo sapiens.
XX OS
XX
XX Key Location/Qualifiers
XX MISC-difference 1..307 /note= "optionally mutated to increase electrostatic
XX interaction between beta hairpin structure and
XX a receptor"
XX Domain 308..328 /label= beta hairpin loop_1
XX /note= "mutant optionally comprises one or more
XX substitutions in these residues"
XX MISC-difference 329..375 /note= "optionally mutated to increase electrostatic
XX interaction between beta hairpin structure and
XX a receptor"
XX Domain 376..400 /label= beta hairpin loop_3
XX /note= "mutant optionally comprises one or more
XX substitutions in these residues"
XX MISC-difference 401..407 /note= "optionally mutated to increase electrostatic
XX interaction between beta hairpin structure and
XX a receptor"
XX
XX MO200017360-A1.
XX PN
XX PD 30-MAR-2000.
XX PP
XX PR 19-MAR-1999; 99MO-US05908.
XX PR 22-SEP-1998; 98MO-US19772.
XX PA (UYMA-) UNIV MARYLAND BALTIMORE.
XX PI Weintrub BD, Szkudlinski MW;
XX DR WPI: 2000-283585/24.

```

```

XX New mutant cysteine knot growth factor proteins comprising one or more
XX mutant subunits, useful for treating or preventing diseases e.g.
XX hypothyroidism and thyroid cancer
XX Claim 328: Page 305; 320pp; English.
XX
XX This is the wild type human activin B subunit.
XX Mutants comprise at least one electrostatic charge altering mutation in a
XX beta hairpin loop, resulting in increased bioactivity.
XX Mutant cysteine knot growth factor (CKGF) proteins comprising one or more
XX mutant subunits and having novel properties or improved pharmacological
XX properties, compared to wild type CKGFs, are claimed. The CKGF
XX superfamily comprises at least four families of growth factors: the
XX glycoprotein hormones, the platelet-derived growth factor (PDGF) family,
XX the neurotrophins and the transforming growth factor-beta family; the
XX families are known to be structurally similar (especially comprising the
XX cysteine knot topology) and it was shown that mutations at certain
XX positions in the CKGF hairpin loops of family members and other members
XX of the CKGF superfamily could significantly alter the biological
XX activities of the CKGF.
XX Mutant transforming growth factor family proteins or analogues are useful
XX for treatment of ovulatory dysfunction, luteal phase defect, unexplained
XX infertility, time-limited conception and in assisted reproduction.
XX
XX Sequence 407 AA:
XX
XX Query Match 32.4%; Score 599.5; DB 21; Length 407;
XX Best Local Similarity 36.6%; Pred No. 1,2e-49;
XX Matches 145; Conservative 60; Mismatches 118; Indels 73; Gaps 16;
XX
XX OY 13 APTVATPRA-----GQD---CPACGGPTLELESOREL-----LIDLAKRSLTD 53
XX Db 29 SPPPPPTPAAPPPPPGSPGSGDCTSGG---FRREBELGVDGDFLEAVKRIHLS 84
XX OY 54 KLHLTOPRLNRPVSRALRTALQHLGVPQCALLEDNR-----EQEC 96
XX Db 85 RLOMRCRPNITHAVPKAAWVTALRLHA---GKVEDRGEVEIPLHLDGASPGADGQERVS 141
XX OY 97 EIISFAETGLSTINOTRLDFHSSDRTAGDRE--VQOASIMFVQLPSNTWTTL----- 148
XX Db 142 EIISFAETDGLASSRRLYEFLISNE--GNOLFFVQAALMLYLKL---LPVLEKGSRR 195
XX OY 149 KVRVLVL---GPHNTNLTATQYLLEVDASGWHQLPLRPEAQAACSGHLLTLEVLGQV 205
XX Db 196 KVRVAVVPEVDGEGHGRMNM-VEKRVDLKRSQWHTFPLTEAIOALEFERGERRLNLDVQCD 254
XX OY 206 AQSIVL-----GGAHREPVAAARVVG-GKHQIHRGIDCGGSRMCCROEFFVDFRE 258
XX Db 255 CQELAVVPEVDGEGHGRMNM-VEKRVDLKRSQWHTFPLTEAIOALEFERGERRLNLDVQCD 314
XX OY 259 IGHWDIITQPEGVAMNFCIGCCPLHAGMPGIAASFHTAVLNLKANPAAGTTGG--GSC 316
XX Db 315 IGHWDIITQPEGVAMNFCIGCCPLHAGMPGIAASFHTAVLNLKANPAAGTTGG--GSC 316
XX OY 317 CVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGCS 352
XX Db 372 CIPTKLSTMSMLYFDEYNIKRDVPMNIVEBCGA 407

RESULT 10
AAV70204
ID AAV70204 standard; protein: 353 AA.
AC AAV70204;
DT 09-APR-1991 (first entry)
XX DE Sequence of human inhibin beta-chain precursor beta-B.
XX Fertility control; contraception; hormone; spermatogenesis.
XX OS Homo sapiens.

```

XX	Key	Location/Qualifiers
XX	Modified-site	38..40
FT		/note="potential N-linked glycosylation sites"
FT	Region	1..237
FT		/note="used to design a long synthetic DNA probe"
FT	Protein	238..343
FT	Cleavage-site	235..237
XX		/note="proteolytic processing site"
PN	EP222491-A.	
XX		
PD	20-MAY-1987.	
XX		
PF	02-OCT-1986;	86EP-0307586.
XX		
PR	12-SEP-1986;	86US-0906729.
PR	03-OCT-1985;	86US-0783910.
PR	10-FEB-1986;	86US-0827710.
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Mason AJ, Seeburg PH;	
XX		
PT	WPI: 1987-137512/20.	
PT	N-PSDB: MANT0316.	
XX		
PT	Recombinant human or porcine inhibin or activin - used for	
PT	modulating clinical condition or reproductive physiology of	
XX	animals.	
XX	Disclosure: Fig 9A: 48pp: English.	
XX		
XX	A compsn. comprising human or porcine inhibin which is claimed	
CC	free of unidentified or porcine proteins is claimed. Also claimed	
CC	are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta	
CC	chain. Sequencing of inhibin-encoding cDNA has led to the	
CC	identification of prodomain regions located N-terminal to the	
CC	mature inhibin chains that represent coordinately expressed	
CC	biologically active polypeptides. The prodomain regions or	
CC	prodomain immunogens are useful in monitoring preproinhibin	
CC	processing in transformant cell culture or in experiments directed	
CC	at modulating the clinical condit. or reproductive physiology of	
CC	animals.	
XX		
XX	Sequence 353 AA;	
SQ		
	Query Match	31.9%; Score 590; DB 8; Length 353;
	Best Local Similarity	37.3%; Pred. No. 8.1e-49;
	Matches 138; Conservative 59; Mismatches 113; Indels 60; Gaps 14;	
QY	26 GPACGPTLELESQREL-----LTDLAKRSTLDKLTQPTLNRPYSRAALRTALQHL 79	
Db	1 CTSCGG-----FRPELGRVGDGDFLEAVKRNHLSRQMGKRNITTHAHPKANVATLRKL 56	
QY	80 HGVPGQALLEDNR-----DQCEIISFAETGSLTINQTRIDHFSSDR 122	
Db	57 HA--GKVRDEGRVEIPHLDGSHASPGADQGERVSEIISFAETDGLASSRVLRFFTSNE 112	
QY	123 TAGDRE--VOOASLMFFQQLPSNTITWL-----KVRVLV---GPHNTLTIAQYILE 171	
Db	113 --GNONLEFVQASLMITLKL--LPTVLEKGSRRKRVKVFQEGCHDDRMN-VEKRYD 166	
QY	172 VDSAGMQLPLGPEAOAACSQHLTLLELVLEGOVQSSVIL-----GGAARPPVAVR 225	
Db	167 LKRGSMHFFPLETALIQALFERGERRLNDVQDSQGLAVVPVADPDEBSHRRPVVQA 226	
QY	226 RVG-GKHDIHRRGIDCCGGRMCRCRQEFVVPFRELGHMDWITIOEGVAMNFCIGCQPLHI 284	
Db	227 RLGSRHRIIRKRGDCQDRNLCCRQGFDFRLIGMDWIMIAIPGYGVCCEGCPAYL 286	
QY	285 AGMDGIASFPTAVLNLKANTAGTTGG--GSCVPTARRPLSLIYDRDSNTVKTDP 342	

Db	287	ACVPGGASSEFHTAVYQVRMR---	GLNDGTNVSCCIFTKLSTMSMLYFPDDEVINYKRDVP	343
QY	343	DMVVEACGCS	352	
		: : :		
Db	344	NMIVECGCA	353	
	RESULT 11			
	AA070201			
ID	AA070201 standard; protein; 351 AA.			
XX	XX			
AC	AA070201;			
XX	XX			
DT	09-APR-1991 (first entry)			
DE	Sequence of porcine inhibin beta-chain precursor beta-B.			
XX	XX			
KW	Fertility control; contraception; hormone; spermatogenesis.			
XX	XX			
OS	Sus scrofa domestica.			
FT	FT			
FT	FT			
FT	FT			
FT	Region			
FT	Location/Qualifiers			
FT	1..270			
FT	/note="used to design a long synthetic DNA probe"			
FT	Protein			
FT	271..386			
FT	Cleavage-site			
FT	268..270			
FT	/note="proteolytic processing site"			
PN	EP222491-A.			
XX	XX			
PD	20-MAY-1987.			
XX	XX			
PF	02-OCT-1986; 86EP-0307586.			
PR	12-SEP-1986; 86US-0906729.			
PR	03-OCT-1985; 85US-0783910.			
PR	10-FEB-1986; 86US-0827710.			
PA	(GETH) GENENTECH INC.			
PI	Mason AJ, Seeburg PH;			
DR	WP1: 1987-137512/20.			
DR	N-PSDB: AAN70318.			
XX	XX			
PT	Recombinant human or porcine inhibin or activin - used for			
PT	modulating clinical condition or reproductive physiology of			
PT	animals.			
PS	Disclosure: Fig 2B: 48pp: English.			
XX	XX			
CC	A compsn. comprising human or porcine inhibin which is completely			
CC	free of unidentified or porcine proteins is claimed. Also claimed			
CC	are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta			
CC	chain. Sequencing of inhibin-encoding cDNA has led to the			
CC	identification of prodomain regions located N-terminal to the			
CC	mature inhibin chains that represent coordinately expressed			
CC	biologically active polypeptides. The prodomain regions or			
CC	prodomain immunogens are useful in monitoring proinhibin			
CC	processing in transformant cell culture or in experiments directed			
CC	at modulating the clinical condit. or reproductive physiology of			
XX	XX			
SO	Sequence 351 AA;			
Query Match	31.3%; Score 578; DB 8; Length 351;			
Best Local Similarity	37.3%; Pred.No. 1,2e-47;			
Matches 128; Conservative 62; Mismatches 111; Indels 42; Gaps				
OY	44 LDLAKSIIIDKHLTRPFLNRPYSRAALRTALOHMGVFGALLDENR-----	92		
	: : : : : :			
Db	17 LEAVKRITLIRLOMRSPNITHAVPKAMAYVALRLIA--GKRVREGRAVIDPHLDGIHAS	73		

OY 93 -----EBCCELISPAETGSLTINOTRLDPHFSSDRTAGDRE--VOOASLMPFVO----- 139
 DB 74 PGADQGEKSEVSEISFAETDGLASSRVRLEYFISNE---GQNLFVVOASLMLTKLLPY 130
 OY 140 LPSNTWTLKRVLYLVGPHNTNLATQYLLVEDASGMHQLPLGPEAOACSGHLLTEL 199
 DB 131 LEKSGRRKRVKRVYFOEGHCDRMDVYKRYDLKRSGMHLLPLLEALQALFERGERLNL 190
 OY 200 VLEGQVQSSVYL-----GGAHRRPVAARVVGK--HQHRRGIDCOGSGRMCROE 251
 DB 191 DVQCCGCELAIVPVFVDPGESHRRPFVVOARLDSRPHRIKRGLECDGRTMLCCROQ 250
 OY 252 FVVDREIGHMWTIOPRGYAMNFCIGCCPLHAGMPGSIASFHTAYLN--LLKANTAG 309
 DB 251 FPIDRLIGMSWMIAPRGYKCYKCEGSPAYLAGVPGSASSFHTAVVNOYRMGLMPFG 310
 OY 310 TTGGGSCCVPTARRPLSLLYDRDSNIYKTDIPDMVVEACGS 352
 DB 311 TV--NSCCIPTKLSTMSMUYFDEYNIYKRDVPMNIVECCGA 351

RESULT 12

AAP70200
 ID AAP70200 standard; protein: 427 AA.

AC AAP70200;

DT 09-APR-1991 (first entry)

DE Sequence of porcine inhibin beta-chain precursor beta-A.

XX Fertility control; contraception; hormone; spermatogenesis.

XX Sus scrofa domestica.

OS Key Location/Qualifiers

XX FH Region 1..308 /note="used to design a long synthetic DNA probe"

FT Protein 309..424

FT Cleavage-site 304..308 /note="proteolytic processing site"

FT EP222491-A.

PN 20-MAY-1987.

XX 02-OCT-1986; 86EP-0307586.

XX 12-SEP-1986; 86US-0906729.

PR 03-OCT-1985; 85US-0783910.

PR 10-FEB-1986; 86US-0827710.

XX (GETH) GENENTECH INC.

XX Mason AJ, Seeburg PH;

XX WPI: 1987-137512/20.

DR N-PSDB; AAN70317.

XX Recombinant human or porcine inhibin or activin - used for

XX modulating clinical condition or reproductive physiology of

XX animals.

XX Disclosure; fig 2B; 48pp; English.

XX A compsn. comprising human or porcine inhibin which is completely

XX free of unidentified or porcine proteins is claimed. Also claimed

XX are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta

XX chain. Sequencing of inhibin-encoding cDNA has led to the

XX identification of prodomain regions located N-terminal to the

XX mature inhibin chains that represent coordinately expressed

XX biologically active polypeptides. The prodomain regions or

XX prodomain immunogens are useful in monitoring preproinhibin

CC processing in transformant cell culture or in experiments directed
 CC at modulating the clinical cond. or reproductive physiology of
 CC animals.

XX Sequence 427 AA;

Query Match 30.2%; Score 558.5; DB 8; Length 427;

Best Local Similarity 31.3%; Pred. No. 1.2e-45;

Matches 132; Conservative 70; Mismatches 141; Indels 79; Gaps 10;

OY 6 LIAFLLAPTVAIPRAC-----QCPACGPTL--ELESORELLDLARSTLDKHL 58
 DB 10 LLASCIWIIYRSSPTPGSGSHAPDCPCALATLPKDVPSOPMVAVKHLLMLHLK 69
 OY 59 ORPTLNRPVSRALTAALQHLH-----GVPGALLDNRDECELISPAET 104
 DB 70 KRDPYTOPPKAALLNAILKLVKGVGENGVLEDDIGRAEKENELMETSILITFAEA 129
 OY 105 GLSTINQRLDFHFS---SDRTAGDREVOOASLMEFVQLPSNTTWTLKRVLYLG----- 156
 DB 130 XGTAXXKRTLREISKESGDSLSV---VERAEIMLFELKVPKANRTKVSIRLEFOQORP 185
 OY 157 -----PHNTNLATQYLLVEDASGMHQLPLGPEAO-----A 188
 DB 186 QGSADAGEAEADYGPPEEKSSEVLISEKVVDAKSTWHLFPVSSITQRLDCKSALDIRT 245
 OY 189 ACSQGHLT-LELVLEGVQVQSSVILIG-----AAHRRPVAARVVGK-- 230
 DB 246 ACQCHETGASLVLLGKKKKKEEAEGRKROEGAGVDEKESHRPTLMQANQSEHP 305
 OY 231 HQHRRGIDCOGSGRMCQEEFVDFREIGHWMIQREGYAMNFCIGCCPLHAGPFI 290
 DB 306 HRRRRRGLECDGKVNICKQKFVFSFKDIGMNDWIAPSGYHANCCEECPSHLAGTSGS 365
 OY 291 AASFHTAVNLKANAATACTGGSCVPTARRPLSLLYDRDSNIYKTDIPDMVVEACG 350
 DB 366 SLSPHSTVINHYMRCHSPANLKSQVPTKLPMMLXYDDGQNIYKIDQNMNIVECCG 425
 OY 351 CS 352
 DB 426 CS 427

RESULT 13

AAP70203
 ID AAP70203 standard; protein: 426 AA.

AC AAP70203;

DT 09-APR-1991 (first entry)

DE Sequence of human inhibin beta-chain precursor beta-A.

XX Fertility control; contraception; hormone; spermatogenesis.

XX Homo sapiens.

XX OS Key Location/Qualifiers

XX FH Modified-site 165..167 /note="potential N-linked glycosylation sites"

FT Region 1..28 /note="signal sequence"

FT Region 28..310 /note="pro region"

FT Protein 306..310 /note="proteolytic processing site"

FT Cleavage-site 306..310

PN EP222491-A.

XX 20-MAY-1987. 86EP-0307586.

Tue Oct 15 13:49:39 2002

us-09-684-383-2.rag

Page 12

Qy 351 CS 352
||
Db 425 CS 426

Search completed: October 12, 2002, 02:06:05
Job time : 43 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 12, 2002, 02:05:12 : Search time 15.5 Seconds

(without alignments)
554.697 Million cell updates/sec

Title: US-09-684-383-2

Perfect score: 1849

Sequence: 1 MNSLLAFLLAPTTVATP.....DSNIVKTDPDMVEACGCS 352

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1: Issued Patents_AA: *
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
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6: /cgn2_6/ptodata/1/1aa/6C.COMB.pep: *

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1849	100.0	352	1	US-08-482-577B-2
2	1849	100.0	352	3	US-08-289-222E-4
3	1849	100.0	352	4	US-09-218-176-2
4	1849	100.0	352	4	US-09-054-526B-4
5	1398	75.6	352	1	US-08-482-577B-4
6	1398	75.6	352	4	US-09-218-176-4
7	664	35.9	350	5	PCT-US95-08745-14
8	664	35.9	350	5	US-08-482-577B-24
9	590	31.9	106	1	US-08-289-222E-28
10	590	31.9	106	4	US-09-218-176-7
11	590	31.9	106	4	US-09-054-526B-28
12	590	31.9	353	1	US-08-197-792-43
13	590	31.9	353	1	US-08-459-850-43
14	590	31.9	353	1	US-08-459-850-43
15	590	31.9	353	1	US-08-459-850-43
16	587	31.7	349	1	US-08-197-792-33
17	587	31.7	349	1	US-08-459-850-33
18	587	31.7	349	1	US-08-459-850-33
19	562	30.4	424	1	US-08-197-792-31
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23	557	30.1	426	1	US-08-459-850-41
24	557	30.1	426	1	US-08-459-850-41
25	457	24.7	127	1	US-08-455-550-11
26	440	23.8	119	2	US-08-274-215A-12
27	440	23.8	119	2	US-08-765-662-12

28	440	23.8	119	4	US-09-184-933-12	Sequence 12, Appl
29	440	23.8	119	5	PCT-US95-08745-12	Sequence 12, Appl
30	391	21.1	128	1	US-08-455-550-12	Sequence 12, Appl
31	389	21.0	147	4	US-08-065-844A-7	Sequence 7, Appl
32	388.5	21.0	121	1	US-08-581-529B-18	Sequence 18, Appl
33	388.5	21.0	121	1	US-08-455-559-24	Sequence 24, Appl
34	388.5	21.0	121	2	US-08-525-596B-28	Sequence 28, Appl
35	388.5	21.0	121	2	US-08-581-528A-18	Sequence 18, Appl
36	388.5	21.0	121	3	US-09-097-616-18	Sequence 18, Appl
37	388.5	21.0	121	3	US-09-177-860A-28	Sequence 28, Appl
38	388.5	21.0	121	4	US-09-145-060-24	Sequence 24, Appl
39	388.5	21.0	121	5	PCT-US94-00557-24	Sequence 24, Appl
40	388.5	21.0	121	5	PCT-US94-07762-18	Sequence 18, Appl
41	388.5	21.0	121	5	PCT-US94-07799-18	Sequence 18, Appl
42	380.5	20.6	120	1	US-08-481-377-22	Sequence 22, Appl
43	380.5	20.6	120	2	US-08-491-835-20	Sequence 20, Appl
44	380.5	20.6	120	3	US-09-153-733A-22	Sequence 22, Appl
45	380.5	20.6	120	3	US-08-946-092A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-482-577B-2
Sequence 2, Application US/08482577B

Patent No. 5807713

GENERAL INFORMATION:

APPLICANT: HOTTEN, GERTRUD

APPLICANT: NEIDHARDT, HELGE

APPLICANT: BECHTOLD, ROLF

APPLICANT: POHL, JENS

TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKAI, KARL, KARLSTEIN, MURRAY, AND ORAM

STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,577B

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KIESNER, SHARON

REGISTRATION NUMBER: 36,335

REFERENCE/DOCKET NUMBER: P564-5010

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-482-577B-2

Query Match 100.0%; Score 1849; DB 1; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.3e-180; Indels 0; Gaps 0;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSLLAFLLAPTTVATPRAAGCGPTLELSORELLDLAKRSILDKLHLTOR 60

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Db 1 MTSLLAFLLAFTTVAATPRAGGCPACGGPTLEESQRELLDLAKRSILDKLHLTOR 60
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Db 61 PTLNRPVSRALRTALQHLHGVPQCALLEDNREDECEITISFAETGLSTINOTRLDPHSS 120
OY 121 DRTAGDREVOQASLMFVQLPSNTTWTLKRVLVLGPHNTNLTLATQYLLEVDASGMHOL 180
Db 121 DRTAGDREVOQASLMFVQLPSNTTWTLKRVLVLGPHNTNLTLATQYLLEVDASGMHOL 180
OY 181 PLGPEAOAACSOGHLLTLELVLEGVAOSSVILGGAHRPFAARVRGKGHQRHRCIDC 240
Db 181 PLGPEAOAACSOGHLLTLELVLEGVAOSSVILGGAHRPFAARVRGKGHQRHRCIDC 240
OY 241 OGGSRMCCROEFFVDREIGMHDWIIQPEGYAMNFCIGQCPHLIAGMPCIAASFHTAVLN 300
Db 241 OGGSRMCCROEFFVDREIGMHDWIIQPEGYAMNFCIGQCPHLIAGMPCIAASFHTAVLN 300
OY 301 LKANTAGTTGGSCCVPTARRPLSLIYDRDSNIYKTDIPDMVVEACGCS 352
Db 301 LKANTAGTTGGSCCVPTARRPLSLIYDRDSNIYKTDIPDMVVEACGCS 352

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RESULT 2

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US-08-289-222E-4
Sequence 4, Application US/08289222E
Patent No. 6120760
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HEIGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY & ORAM
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,222E
FILING DATE: 25-AUG-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTIS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 4:

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SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-289-222E-4

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Query Match 100.0%; Score 1849; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 1,3e-180;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MTSLLAFLLAFTTVAATPRAGGCPACGGPTLEESQRELLDLAKRSILDKLHLTOR 60
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Db 61 PTLNRPVSRALRTALQHLHGVPQCALLEDNREDECEITISFAETGLSTINOTRLDPHSS 120
OY 121 DRTAGDREVOQASLMFVQLPSNTTWTLKRVLVLGPHNTNLTLATQYLLEVDASGMHOL 180
Db 121 DRTAGDREVOQASLMFVQLPSNTTWTLKRVLVLGPHNTNLTLATQYLLEVDASGMHOL 180
OY 181 PLGPEAOAACSOGHLLTLELVLEGVAOSSVILGGAHRPFAARVRGKGHQRHRCIDC 240
Db 181 PLGPEAOAACSOGHLLTLELVLEGVAOSSVILGGAHRPFAARVRGKGHQRHRCIDC 240
OY 241 OGGSRMCCROEFFVDREIGMHDWIIQPEGYAMNFCIGQCPHLIAGMPCIAASFHTAVLN 300
Db 241 OGGSRMCCROEFFVDREIGMHDWIIQPEGYAMNFCIGQCPHLIAGMPCIAASFHTAVLN 300
OY 301 LKANTAGTTGGSCCVPTARRPLSLIYDRDSNIYKTDIPDMVVEACGCS 352
Db 301 LKANTAGTTGGSCCVPTARRPLSLIYDRDSNIYKTDIPDMVVEACGCS 352

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RESULT 3

```

US-09-218-176-2
Sequence 2, Application US/09218176
Patent No. 6171584
GENERAL INFORMATION:
APPLICANT: H TTEN, Gertrud
APPLICANT: NEIDHARDT, Heige
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, Jens
APPLICANT: PAULISTA, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., G Street Lobby,
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218,176
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,048
FILING DATE: 12-JUL-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03065

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FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 2-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,577
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92 102 324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 11 243.1
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: KITTIS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-6010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-218-176-2

Query Match 100.0%; Score 1849; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.3e-180; Mismatches 0; Indels 0; Gaps 0;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MTSLLLAFLAPTTVATPRAGGCPACGPTLEESORELLDLAKRSILDKLHLTOR 60
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DB 61 PTLNRPVSRAALTAOLHAGVPOGALLDNRBOCEIISFAETGLSTINOTRLDFHSS 120
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DB 121 DRTAGREVOQASLMEFVQLPSMTTTLKRVYLVLGPHNTNLTATQYLLEVDASGMHQL 180
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DB 181 PLGPEAOAACSOGHLLTLELVLEGOVAVSSVILGGAHRRPFVAVRVGKGHIHRRGIDC 240
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DB 241 OGGSRMCCROEFVDFREIGMHMTIOPRGYAMNFCIGCPLHIGMGIASFTTAVLN 300
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DB 301 LKANTAGTTGGGSCCVPTARRPLSLYYDRDSNIVKTDIDPMVVEACGCS 352

RESULT 4
US-09-054-526B-4
; Sequence 4, Application US/09054526B
; Patent No. 6197550
; GENERAL INFORMATION:
; APPLICANT: H TTEEN, GERTHARD
; APPLICANT: NEIDHARDT, HELGE
; APPLICANT: BECHTOLD, ROLF
; APPLICANT: POHL, JENS
; TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
; GROWTH/DIFFERENTIATION FACTORS
; NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
CITY: WASHINGTON
STATE: DC

COUNTRY: USA
ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,526B
FILING DATE: 03-APR-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993

ATTORNEY/AGENT INFORMATION:
NAME: KITTIS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-8005

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-054-526B-4

Query Match 100.0%; Score 1849; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.3e-180; Mismatches 0; Indels 0; Gaps 0;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSLLLAFLAPTTVATPRAGGCPACGPTLEESORELLDLAKRSILDKLHLTOR 60
DB 1 MTSLLLAFLAPTTVATPRAGGCPACGPTLEESORELLDLAKRSILDKLHLTOR 60
QY 61 PTLNRPVSRAALTAOLHAGVPOGALLDNRBOCEIISFAETGLSTINOTRLDFHSS 120
DB 61 PTLNRPVSRAALTAOLHAGVPOGALLDNRBOCEIISFAETGLSTINOTRLDFHSS 120
QY 121 DRTAGREVOQASLMEFVQLPSMTTTLKRVYLVLGPHNTNLTATQYLLEVDASGMHQL 180
DB 121 DRTAGREVOQASLMEFVQLPSMTTTLKRVYLVLGPHNTNLTATQYLLEVDASGMHQL 180
QY 181 PLGPEAOAACSOGHLLTLELVLEGOVAVSSVILGGAHRRPFVAVRVGKGHIHRRGIDC 240
DB 181 PLGPEAOAACSOGHLLTLELVLEGOVAVSSVILGGAHRRPFVAVRVGKGHIHRRGIDC 240
QY 241 OGGSRMCCROEFVDFREIGMHMTIOPRGYAMNFCIGCPLHIGMGIASFTTAVLN 300
DB 241 OGGSRMCCROEFVDFREIGMHMTIOPRGYAMNFCIGCPLHIGMGIASFTTAVLN 300
QY 301 LKANTAGTTGGGSCCVPTARRPLSLYYDRDSNIVKTDIDPMVVEACGCS 352
DB 301 LKANTAGTTGGGSCCVPTARRPLSLYYDRDSNIVKTDIDPMVVEACGCS 352

RESULT 5
US-08-482-577B-4
Sequence 4, Application US/08482577B
Patent No. 5807713
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY, AND ORAM
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,
SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,577B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, SHARON
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P564-5010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
DOCUMENT NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
US-08-482-577B-4

Query Match 75.6%; Score 1398; DB 1; Length 352;
Best Local Similarity 76.2%; Pred. No. 1,4e-134;
Matches 269; Conservative 32; Mismatches 30; Indels 2; Gaps 2;

QY 1 MTSLLAFLAFLAAPTVAAPRAGGCPACGPPYLESONELLDLAKSIIDKLHLTOR 60
DB 1 MASSLLALLFLPTTVVNVKTEGPPACGALFEDLESORELLDLAKSIIDKLHLTOR 60
QY 61 PTLNRPVSRAALTAOLHGVQALL- DNEQCEIISFRETSLTINOTRLDFHRS 119
DB 61 PLSRPVSRAALTAOLHGVQALL- DNEQCEIISFRETSLTINOTRLDFHRS 119
QY 120 SDRTAGDREVOAASLAFVQULPNTWTMLKRVLYLGPHNTNTLTATOVLLVEDASGMO 179
DB 121 G-RMAGSMEVROTREFRPFQVFPINATOTMIRVLRPDTNTLTLSQYVVVNASGMO 179
QY 180 LPLGPEAOAASGSHLTLELVLEGQVASSVILGNAHBPFAARVVGKIHHRGID 239
DB 180 LPLGPEAOAASGSHLTLELVLEGQVASSVILGNAHBPFAARVVGKIHHRGID 239
QY 240 CCGSRRCCROEFVDFRELGMDIITQEGYAMNCTOCPLHLAGMGIAASFTAVL 299
DB 240 CCGSRRCCROEFVDFRELGMDIITQEGYAMNCTOCPLHLAGMGIAASFTAVL 299
QY 300 NLKANTAACTGGGSCVPTARPLSLLYDRDSNIVTDTIDPMVVEACGCS 352

Db 300 NLKANTAACTGGGSCVPTARPLSLLYDRDSNIVTDTIDPMVVEACGCS 352

RESULT 6
US-09-218-176-4
Sequence 4, Application US/09218176
Patent No. 6171584
GENERAL INFORMATION:
APPLICANT: HOTTEN, Gertrud
APPLICANT: NEIDHARDT, Helge
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, Jens
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
TITLE OF INVENTION: TGF- FAMILY
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N.W., G Street Lobby,
SUITE 330
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218,176
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,048
FILING DATE: 12-JUL-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03065
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 2-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,577
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92 102 324, 8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190,3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 11 243,1
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: KITS, Monica Chln
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-6010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-218-176-4

Query Match 75.6%; Score 1398; DB 4; Length 352;

Best Local Similarity 76.28; Pred. No. 1,4e-134;
Matches 269; Conservative 32; Mismatches 50; Indels 2; Gaps 2;

OY 1 MTSLLAFLLAFTTAVTPRAGGCPACGPPTELESORELLDLAKRSITDLKLTOR 60
1 MASSLLALFLPTTYVNPKEGCPACMGAFPLESORELLDLAKRSITDLKLTOR 60
DB 61 PTLNRPVSAALRTALQHLHGVGALL-DNRECEIISFAETGISTINOTRLDPHS 119
61 PTLNRPVSAALRTALQHLHGVGALL-DNRECEIISFAETGISTINOTRLDPHS 120
DB 61 PTLNRPVSAALRTALQHLHGVGALL-DNRECEIISFAETGISTINOTRLDPHS 120
OY 120 SDRTAGDEVOOASLMFFVQPLPSNTTTLKAVIVLGHNTNLTALQYLEVNASGHW 179
121 G-RMAGMEVROTREMFFVQFPHNATOTMNTNVLRLPYDTNLTSTQYVQVNASGHW 179
DB 180 LPLGPAQAACSGHLLTLELVGOVAAOSSVILGGAH-RPEVAARVVGKHOIHRGID 239
180 LPLGPAQAACSGHLLTLELVGOVAAOSSVILGGAH-RPEVAARVVGKHOIHRGID 239
DB 180 LPLGPAQAACSGHLLTLELVGOVAAOSSVILGGAH-RPEVAARVVGKHOIHRGID 239
OY 240 CQGSRMCCROEFVDFREIGWHDWIOPEGYAMNFCIGCPLHAGPGTAASTHTAVL 299
240 CQGSRMCCROEFVDFREIGWHDWIOPEGYAMNFCIGCPLHAGPGTAASTHTAVL 299
DB 240 CQGSRMCCROEFVDFREIGWHDWIOPEGYAMNFCIGCPLHAGPGTAASTHTAVL 299
OY 300 NLKANTAGCTGGSCCVPTARPLSLIYDRDSNIYVTDIPDMVVEACGS 352
300 NLKANTAGCTGGSCCVPTARPLSLIYDRDSNIYVTDIPDMVVEACGS 352
DB 300 NLKANTAGCTGGSCCVPTARPLSLIYDRDSNIYVTDIPDMVVEACGS 352

RESULT 7
US-08-765-662-14

; Sequence 14, Application US/08765662

; Patent No. 5928213

; GENERAL INFORMATION:

; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/765,662

; FILING DATE: 28-APR-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA: PCT/US95/08745

; FILING DATE: 12-JUL-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Halle, Ph.D., Lisa A

; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 07265/042M01 (FD-3830)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-678-5070

; TELEFAX: 619-678-5099

; TELEX:

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 350 amino acids

; TYPE: amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: Internal

; ORIGINAL SOURCE:
US-08-765-662-14

Query March 35.98; Score 664; DB 2; Length 350;

Best Local Similarity 43.38; Pred. No. 1,1e-59;

Matches 156; Conservative 52; Mismatches 118; Indels 34; Gaps 14;

OY 9 FILLAPPTVATPRAGGCPACGPPTELESORELLDLAKRSITDLKLTORPLNRPVS 68
9 FILLAPPTVATPRAGGCPACGPPTELESORELLDLAKRSITDLKLTORPLNRPVS 68
DB 9 FILLAPPTVATPRAGGCPACGPPTELESORELLDLAKRSITDLKLTORPLNRPVS 68
OY 69 RAALFTALQHLHGVGALL-DNRECEIISFAE-TGLSTINOTRLDPHSSDRTAGDR 127
69 RAALFTALQHLHGVGALL-DNRECEIISFAE-TGLSTINOTRLDPHSSDRTAGDR 127
DB 69 RAALFTALQHLHGVGALL-DNRECEIISFAE-TGLSTINOTRLDPHSSDRTAGDR 127
OY 128 EVOOASLMFFVQPLPSNTTTLKAVIVLGHNTNLTALQYLEVNASGHWPLG 183
128 EVOOASLMFFVQPLPSNTTTLKAVIVLGHNTNLTALQYLEVNASGHWPLG 183
DB 128 EVOOASLMFFVQPLPSNTTTLKAVIVLGHNTNLTALQYLEVNASGHWPLG 183
OY 184 PEAQAACSGHLLTLELVGOVAAOSSVILGGAH-RPEVAARVVGKHOIHRGID 234
184 PEAQAACSGHLLTLELVGOVAAOSSVILGGAH-RPEVAARVVGKHOIHRGID 234
DB 184 PEAQAACSGHLLTLELVGOVAAOSSVILGGAH-RPEVAARVVGKHOIHRGID 234
OY 175 SSGLRKSGSVLKLQDCRPLEGNSYVGOPRRLDTAGHQPFLEIKRANEDGAGAR 234
175 SSGLRKSGSVLKLQDCRPLEGNSYVGOPRRLDTAGHQPFLEIKRANEDGAGAR 234
DB 175 SSGLRKSGSVLKLQDCRPLEGNSYVGOPRRLDTAGHQPFLEIKRANEDGAGAR 234
OY 235 RRGIDCGSRMCCROEFVDFREIGWHDWIOPEGYAMNFCIGCPLHAGPGTAASTHTAVL 294
235 RRGIDCGSRMCCROEFVDFREIGWHDWIOPEGYAMNFCIGCPLHAGPGTAASTHTAVL 294
DB 235 RRGIDCGSRMCCROEFVDFREIGWHDWIOPEGYAMNFCIGCPLHAGPGTAASTHTAVL 294
OY 295 HTAVNLKANT--AGCTGGSCCVPTARPLSLIYDRDSNIYVTDIPDMVVEACGS 352
295 HTAVNLKANT--AGCTGGSCCVPTARPLSLIYDRDSNIYVTDIPDMVVEACGS 352
DB 295 HTAVNLKANT--AGCTGGSCCVPTARPLSLIYDRDSNIYVTDIPDMVVEACGS 352

RESULT 8
PCT-US95-08745-14

; Sequence 14, Application PC/TUS9508745

; GENERAL INFORMATION:

; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/08745

; FILING DATE: 12-JUL-1995

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Halle, Ph.D., Lisa A

; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 07265/042M01 (FD-3830)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-678-5070

; TELEFAX: 619-678-5099

; TELEX:

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 350 amino acids

; TYPE: amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: Internal

ORIGINAL SOURCE:
PCT-US95-08745-14

Query Match 35.9%; Score 664; DB 5; Length 350;
Best Local Similarity 43.3%; Pred. No. 1,1e-59;
Matches 156; Conservative 52; Mismatches 118; Indels 34; Gaps 14;

OY 9 FLLAPTYATPRACGCGPACGCGPTLESGRELLDLAKRSILDKLTLTORPTLNKRV 68
DB 9 WLVLLMALVRAQGTGSCVPCGSGSLAPQAEALRYLLEAKQIIDLGLHSRPRITPP 68
OY 69 RAALRTALOHGVPQALLEDNREQBEELISFAE-TGLSTINOTRDLFFSSDRTAGDR 127
DB 69 QALTRALRRLO---PGSAVAGNE---EVSFAVTYDTSAYSSLLTFHLSIPRS---H 119
OY 128 EYQOASLMEFYQVQLPSNTTTLKRVLYLGP---HNTNLTLAQYLLLEVASCMHOLPIG 183
DB 120 HLYHARLWLHV-LPT-LPGTLCLRFHNGPRRRRQSGRTLLAEHHTNL---GMHTLTL 174
OY 184 PEAOACSGHLLTEL---VLEGO---VAQSVTLGGAH-REPVAARVGV--GRHQIH 234
DB 175 SSGLRGKSGVLLKQLDCLRPLEGNSTYTGPRRLDTPAGHQPFLEIKIRANFGAGRAR 234
OY 235 RRGIDCGGSHMCCROEFFVDFRIGWHDMITIOPEGYAMNFCIGCCPLHAGMPGIAASF 294
DB 235 RRTPTCEPATPLCCRRDHVDFOLGMRDITLOPEGYQLWCGGCPHLAGSPGIAASF 294
OY 235 HTAVNLILKANT--AGTTGGGSCCVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGCS 352
DB 295 HSAVFSLKANNPMPAST---SCCVPTARRPLSLLYLDHNGVYVTDVPMVVEACGCS 350

RESULT 9

US-08-482-577B-24
Sequence 24, Application US/08482577B
Patent No. 5807713

GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIKAI DO, MARIELSTEIN, MURRAY, AND ORAM
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,
STREET: SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,577B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, SHARON
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P664-5010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: Linear
MOLECULE TYPE: peptide
US-08-482-577B-24

Query Match 31.9%; Score 590; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.3e-53;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 247 CCROEFFVDFRIGWHDMITIOPEGYAMNFCIGCCPLHAGMPGIAASFHTAVNLILKANT 306
DB 1 CCROEFFVDFRIGWHDMITIOPEGYAMNFCIGCCPLHAGMPGIAASFHTAVNLILKANT 60
OY 307 AAGTTGGGSCCVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGCS 352
DB 61 AAGTTGGGSCCVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGCS 106

RESULT 10

US-08-289-222E-28
Sequence 28, Application US/08289222E
Patent No. 6120760

GENERAL INFORMATION:

APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIKAI DO, MARIELSTEIN, MURRAY & ORAM
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,222E
CLASSIFICATION: 424
FILING DATE: 25-AUG-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P664-9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-289-222E-28

Query Match 31.9%; Score 590; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.3e-53;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

247 CCRQEFFVDFREIGMHWITIOPEGYAMNFCIGCPLHAGMGIASFTAVLNKANT 306
1 CCRQEFFVDFREIGMHWITIOPEGYAMNFCIGCPLHAGMGIASFTAVLNKANT 60

307 AAGTTGGSCCVPTARRPLSLYYDRDSNIVKTDIPDMVVEACGS 352
61 AAGTTGGSCCVPTARRPLSLYYDRDSNIVKTDIPDMVVEACGS 106

RESULT 11

US-09-218-176-7

Sequence 7, Application US/09218176

Patent No. 6171584

GENERAL INFORMATION:

APPLICANT: HITTEN, Gertrud

APPLICANT: NEIDHARDT, Helge

APPLICANT: BECHTOLD, Rolf

APPLICANT: POHL, Jens

APPLICANT: PAULISTA, Michael

TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE

TITLE OF INVENTION: TGF- FAMILY

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKAIKO, MARMELESTEIN, MURRAY & ORAM LLP

STREET: 655 Fifteenth Street, N. W., G Street Lobby,

STREET: Suite 330

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/218,176

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/679,048

FILING DATE: 12-JUL-1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP96/03065

FILING DATE: 12-JUL-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00350

FILING DATE: 2-FEB-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/482,577

FILING DATE: 7-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92 102 324.8

FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 23 190.3

FILING DATE: 01-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 195 11 243.1

FILING DATE: 27-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: KITTIS, MONICA CHIN

REGISTRATION NUMBER: 36,105

REFERENCE/DOCKET NUMBER: P564-6010

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-218-176-7

Query Match 31.9%; Score 590; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.3e-53;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

247 CCRQEFFVDFREIGMHWITIOPEGYAMNFCIGCPLHAGMGIASFTAVLNKANT 306
1 CCRQEFFVDFREIGMHWITIOPEGYAMNFCIGCPLHAGMGIASFTAVLNKANT 60

307 AAGTTGGSCCVPTARRPLSLYYDRDSNIVKTDIPDMVVEACGS 352
61 AAGTTGGSCCVPTARRPLSLYYDRDSNIVKTDIPDMVVEACGS 106

RESULT 12

US-09-054-5268-28

Sequence 28, Application US/090545268

Patent No. 6197550

GENERAL INFORMATION:

APPLICANT: HITTEN, GERTRUD

APPLICANT: NEIDHARDT, HELGE

APPLICANT: BECHTOLD, ROLF

APPLICANT: POHL, JENS

TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL

TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKAIKO, MARMELESTEIN, MURRAY & ORAM LLP

STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,

STREET: SUITE 330

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/054,5268

FILING DATE: 03-APR-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/289,222

FILING DATE: 12-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 23 190.3

FILING DATE: 01-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EPO 92102324.8

FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00350

FILING DATE: 12-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: KITTIS, MONICA CHIN

REGISTRATION NUMBER: 36,105

REFERENCE/DOCKET NUMBER: P564-8005

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-054-526B-28

Query Match 31.9%; Score 590; DB 4; Length 106;
 Best Local Similarity 100.0%; Pred. No. 7.3e-53;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 CCRQEFFVDFREIGHMDHTIOPEGAMNFCIGGCPHLAGMPTAASHTAVLMLKANT 306
 DB 1 CCRQEFFVDFREIGHMDHTIOPEGAMNFCIGGCPHLAGMPTAASHTAVLMLKANT 60
 QY 307 AAGTTGGGSCCVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGCS 352
 DB 61 AAGTTGGGSCCVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGCS 106

RESULT 13
 US-08-197-792-43

Sequence 43, Application US/08197792
 Patent No. 5525488

GENERAL INFORMATION:
 APPLICANT: Anthony J. Mason
 APPLICANT: Peter H. Seeburg
 TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or Beta Chains of Inhibin and
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/197, 792
 FILING DATE: 16-FEB-1994

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/958414
 FILING DATE: 08-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/744207
 FILING DATE: 12-AUG-1991

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/215466
 FILING DATE: 05-JUL-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 06/906729
 FILING DATE: 31-DEC-1986

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 06/827710
 FILING DATE: 07-FEB-1986
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 06/783910
 FILING DATE: 03-OCT-1985

ATTORNEY/AGENT INFORMATION:
 NAME: Hasak, Janet E.
 REGISTRATION NUMBER: 28,616
 REFERENCE/DOCKET NUMBER: 297P204
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1896
 TELEFAX: 415/952-9881

TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 353 amino acids
 TYPE: amino acid

TOPOLOGY: linear
 US-08-197-792-43

Query Match 31.9%; Score 590; DB 1; Length 353;
 Best Local Similarity 37.3%; Pred. No. 4e-52;
 Matches 138; Conservative 59; Mismatches 113; Indels 60; Gaps 14;

QY 26 CCRQEFFVDFREIGHMDHTIOPEGAMNFCIGGCPHLAGMPTAASHTAVLMLKANT 79
 DB 1 CCRQEFFVDFREIGHMDHTIOPEGAMNFCIGGCPHLAGMPTAASHTAVLMLKANT 56
 QY 80 HGVPOGALLEDR-----BOCEIISFAETGISTINQRLDHFHSSDR 122
 DB 57 HA---GKVRQEDQVETIPLDGHASGADGQERVSEIISFAETGGLASSRVRKLEFFISNE- 112
 QY 123 TAGDRE--VQASLMFEVQPLPSNTTWL-----KVRVLV---GPHNTULATGYLLE 171
 DB 113 --GNQNLFFVQASLMYLYKL--LPVLEKGRKRVKRVKVFQDQGHGDKMMN-VEKRD 166
 QY 172 VDASGHQDLPLPEQVQACSGHITLVLVLEGVQVSSVLL-----GCAHRPVAARV 225
 DB 167 LRRSGMHTFPLTEAIOALFERGERRLNDVQCCSCDELAVVPVDPGESHRPFVVOA 226
 QY 226 RVG-GKHQIHRGIDCOGSHRCCROEFFVDFREIGHMDHTIOPEGAMNFCIGGCPH 284
 DB 227 RLGDGRHRIKRGLECGGRTMLCCROQFIDRLIGNMDIITPTGYNYCGSCPAVL 286
 QY 285 AGMPTAASHTAVLMLKANTAGTTGG--GSCVPTARRPLSLLYDRDSNIVKTDIP 342
 DB 287 AGVPSASSFHTAVVNOYRMR---GLNPCTVNSCIPTKLSTMSMLYFQDEYNIVKRDVP 343
 QY 343 DMVVEACGCS 352
 DB 344 NMVVECCGA 353

RESULT 14
 US-08-459-850-43

Sequence 43, Application US/08459850
 Patent No. 5665568

GENERAL INFORMATION:
 APPLICANT: Anthony J. Mason
 APPLICANT: Peter H. Seeburg
 TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
 TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypept
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459, 850
 FILING DATE: 02-JUN-1995

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/197792
 FILING DATE: 17-FEB-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/958414
 FILING DATE: 08-OCT-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/744207
 FILING DATE: 12-AUG-1991
 PRIOR APPLICATION DATA:

TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 353 amino acids
 TYPE: amino acid

APPLICATION NUMBER: 07/215466
 FILING DATE: 05-JUL-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 06/906729
 FILING DATE: 31-DEC-1986
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 06/827710
 FILING DATE: 07-FEB-1986
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 06/783910
 FILING DATE: 03-OCT-1985
 ATTORNEY/AGENT INFORMATION:
 NAME: Hasak, Janet E.
 REGISTRATION NUMBER: 28, 616
 REFERENCE/DOCKET NUMBER: 297P2D5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1896
 TELEFAX: 415/952-9881
 TELETYPE: 910/371-7168
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 353 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-459-850-43

Query Match 31.9%; Score 590; DB 1; Length 353;
 Best Local Similarity 37.3%; Pred. No. 4e-52;
 Matches 138; Conservative 59; Mismatches 113; Indels 60; Gaps 14;

QY 26 CPACGGPTLELESOREL-----LLDLAKRSIIDKLHLTORPTLNRPVRAALRTALQHL 79
 DB 1 CTSCGG-----FRPEELGRVDGDFLEAVKRIILSRLOMRGRPNITAVPRAAAVTAALRL 56
 QY 80 HGVPOGALLEENR-----EOCEIISFAETGLSTINOTRIDPHRSSDR 122
 DB 57 HA---GKVEDEGRVETPHLDGHSFGADGGERVSEIISFAETGLASSRRLVLEFFISNE 112
 QY 123 TAGDRE--VOQASLMFVQLPSNTTWTL-----KVRVLV---GPHNTMLTATQYLE 171
 DB 113 --GNONLFVVOQASIMLYLKL---LPYVLEKGSRRKRVKVFQDQGHGRNMN-VERKVD 166
 QY 172 VDASGWHOLPLGPEAOACSGHLLLELVLEGQVAVSSVL-----GGAHRPVAARY 225
 DB 167 LKRSQMHFTPLTEALQALFERGERRLNDVQDSCQELAVVPVDPGSESHRPVYVQA 226
 QY 226 RVG-GKHQIHRRGIDCGGSRMCCROEFVDFREIGMHMDIIOEGYAMNFCIGCCPLHI 284
 DB 227 RLGDSRHRIIRKRGLECDGRTNLCRCROOFFIDRLIGNMDWIAPTYGYGNYCEGSCPAYL 286
 QY 285 ACPGIAASFRTAVNLKANTAAAGTTGG--GSCCVTPARRPSSLVYDDSDSNIVKTDIP 342
 DB 287 ACVPSSASSFTAVVNOYRMR---GLNPGTVNSCCIPKLISTMSMLYFDDDEYNIVKRDVP 343
 QY 343 DMVVEACGS 352
 DB 344 NMIVEBCGA 353

RESULT 15
 US-08-459-214-43
 Sequence 43, Application US/08459214
 Patent No. 5716810
 GENERAL INFORMATION:
 APPLICANT: Anthony J. Mason
 APPLICANT: Peter H. Seeburg
 TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
 Beta Chains of Inhibin and Method for Synthesizing Polypeptide
 TITLE OF INVENTION: Using such Nucleic Acid
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd

CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459, 214
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/197792
 FILING DATE: 17-FEB-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/958414
 FILING DATE: 08-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/744207
 FILING DATE: 12-AUG-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/215466
 FILING DATE: 05-JUL-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 06/906729
 FILING DATE: 31-DEC-1986
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 06/827710
 FILING DATE: 07-FEB-1986
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 06/783910
 FILING DATE: 03-OCT-1985
 ATTORNEY/AGENT INFORMATION:
 NAME: Hasak, Janet E.
 REGISTRATION NUMBER: 28, 616
 REFERENCE/DOCKET NUMBER: 297P2D6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1896
 TELEFAX: 415/952-9881
 TELETYPE: 910/371-7168
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 353 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-459-214-43

Query Match 31.9%; Score 590; DB 1; Length 353;
 Best Local Similarity 37.3%; Pred. No. 4e-52;
 Matches 138; Conservative 59; Mismatches 113; Indels 60; Gaps 14;

QY 26 CPACGGPTLELESOREL-----LLDLAKRSIIDKLHLTORPTLNRPVRAALRTALQHL 79
 DB 1 CTSCGG-----FRPEELGRVDGDFLEAVKRIILSRLOMRGRPNITAVPRAAAVTAALRL 56
 QY 80 HGVPOGALLEENR-----EOCEIISFAETGLSTINOTRIDPHRSSDR 122
 DB 57 HA---GKVEDEGRVETPHLDGHSFGADGGERVSEIISFAETGLASSRRLVLEFFISNE 112
 QY 123 TAGDRE--VOQASLMFVQLPSNTTWTL-----KVRVLV---GPHNTMLTATQYLE 171
 DB 113 --GNONLFVVOQASIMLYLKL---LPYVLEKGSRRKRVKVFQDQGHGRNMN-VERKVD 166
 QY 172 VDASGWHOLPLGPEAOACSGHLLLELVLEGQVAVSSVL-----GGAHRPVAARY 225
 DB 167 LKRSQMHFTPLTEALQALFERGERRLNDVQDSCQELAVVPVDPGSESHRPVYVQA 226
 QY 226 RVG-GKHQIHRRGIDCGGSRMCCROEFVDFREIGMHMDIIOEGYAMNFCIGCCPLHI 284
 DB 227 RLGDSRHRIIRKRGLECDGRTNLCRCROOFFIDRLIGNMDWIAPTYGYGNYCEGSCPAYL 286

Tue Oct 15 13:49:39 2002

us-09-684-383-2.rai

Page 10

OY 285 AGMPGTASFFHTAVLNLKANTAGTGG--GSCCVPTARRPLSLYYDRDSNIVKTDIP 342
DB 287 AGVPGSASSFFHTAVVNOYRMR---GLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVP 343
OY 343 DMVVEACGCS 352
DB 344 NMIVECGCA 353

Search completed: October 12, 2002, 02:10:48
Job time : 17.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 12, 2002, 01:13:12 ; Search time 27 Seconds
(without alignments)
1252.720 Million cell updates/sec

Title: US-09-684-383-2

Perfect score: 1849
Sequence: 1 MTSLLAFLLAPTTVA...DSNVKTDIPDMVEAGCS 352

Scoring table: BL0SUM62
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR-71:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1849	100.0	352	2 JC2466	inhibin beta-C cha
2	1398	75.6	352	2 JC5366	activin beta-C - m
3	1392	75.3	352	2 S70360	activin beta C pre
4	688.5	37.2	367	2 JC4151	activin beta D cha
5	648	35.0	350	2 JC5241	activin beta E cha
6	607.5	32.9	370	2 I51199	activin beta B sub
7	605	32.7	408	2 S50899	betab inhibin prec
8	599.5	32.4	407	1 M40150	inhibin beta-B cha
9	595.5	32.2	411	2 B41398	inhibin beta-B cha
10	587	31.7	349	1 WPGGB	inhibin beta-B cha
11	573.5	31.0	393	2 I50103	activin beta B - 2
12	562	30.4	424	1 WPGGBA	inhibin beta-A cha
13	559	30.2	424	1 S31440	inhibin beta-A cha
14	557	30.1	426	1 B24248	inhibin beta-A cha
15	556.5	30.1	425	1 S50898	inhibin beta-A cha
16	552.5	29.9	425	1 I47072	inhibin beta-A cha
17	552	29.9	424	1 B40905	activin beta-A cha
18	547	29.6	413	2 JC4862	inhibin beta-A cha
19	476	25.7	255	2 I48235	inhibin beta-B cha
20	353	19.1	115	2 PNO505	activin beta B-1 C
21	351	19.0	115	2 PNO506	activin beta B-2 C
22	345	17.6	115	2 PNO504	inhibin beta-A cha
23	307.5	16.6	101	2 C36192	inhibin beta-B2 ch
24	306.5	16.6	101	2 B36192	inhibin beta-B1 ch
25	284.5	15.4	393	2 S37073	bone morphogenetic
26	284	15.4	396	1 BMH02	bone morphogenetic
27	282	15.3	102	2 A36192	inhibin beta-A cha
28	281	15.2	394	2 S45355	bone morphogenetic
29	277	15.0	373	2 PM0042	activin - fruit fl

30	267	14.4	357	2 A39364	GDF-1 embryonic gr
31	261	14.1	398	2 JH0688	bone morphogenetic
32	253	13.7	372	2 C39364	GDF-1 embryonic gr
33	247	13.4	398	2 JH0687	bone morphogenetic
34	246.5	13.3	353	2 I50607	bone morphogenetic
35	240	13.0	408	2 S58791	bone morphogenetic
36	239.5	13.0	313	2 I51284	bone morphogenetic
37	237	12.8	402	2 A45056	osteogenic protein
38	237	12.8	402	2 A54798	vg-1-related prote
39	236.5	12.8	405	2 I50608	bone morphogenetic
40	235	12.7	513	1 BMH06	bone morphogenetic
41	231.5	12.5	408	1 BMH04	cet-1 protein - Ca
42	231	12.5	365	2 T43286	bone morphogenetic
43	231	12.5	408	2 S38343	bone morphogenetic
44	230.5	12.5	401	2 JH0689	bone morphogenetic
45	229.5	12.4	426	2 JH0690	bone morphogenetic

ALIGNMENTS

RESULT 1

JC2466
Inhibin beta-C chain precursor - human
N:Alternate names: activin beta C chain
C:Species: Homo sapiens (man)
C:Date: 29-Mar-1995 #sequence_revision 26-May-1995 #text_change 29-Oct-1999
R:Accession: JC2466
R:Host: Gen. Neidhardt, H.; Schneider, C.; Pohl, J.
Biochem. Biophys. Res. Commun. 206, 608-613, 1995
A>Title: Cloning of a new member of the TGF-beta family: A putative new activin betac
A:Reference number: JC2466; MIM:95126961
A:Accession: JC2466
A:Molecule type: mRNA
A:Residues: 1-352 <HOE>
A:Cross-references: GB:X82540; NID:9669154; PIDN:CA57890.1; PID:9669155
A:Experimental source: liver
A:Gene: GDB:INHBC
A:Cross-references: GDB:632884
A:Map position: 2cen-2q13
C:Superfamily: inhibin
C:Keywords: glycoprotein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-236/Domain: propeptide #status predicted <PRO>
F:237-352/Product: activin beta C #status predicted <MAT>
F:110,143,161/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	100.0%	Score 1849	DB 2	Length 352
Best Local Similarity	100.0%	Pred. No. 6.5e-159		
Matches 352	Conservative	0	Mismatches 0	Indels 0
			Gaps 0	
OY	1	MTSLLAFLLAPTTVA	PPRAGGCPACGGPTLEESORELLDLAKRSILDKLHTOR	60
DB	1	MTSLLAFLLAPTTVA	PPRAGGCPACGGPTLEESORELLDLAKRSILDKLHTOR	60
OY	61	PTLNPVSRAALRTAL	LOHLHGYPGALLLEDRBQCELTISAEFGSLSTINOTRLDPFSS	120
DB	61	PTLNPVSRAALRTAL	LOHLHGYPGALLLEDRBQCELTISAEFGSLSTINOTRLDPFSS	120
OY	121	DRPAGREVQASLMP	VOLOPSTNTWTLKRVLYLGPNMTLTLATQYLLLEVDASGHWOL	180
DB	121	DRPAGREVQASLMP	VOLOPSTNTWTLKRVLYLGPNMTLTLATQYLLLEVDASGHWOL	180
OY	181	PLGPEAQAASOGH	LTLELVLEGQVAAQSSVILGGAHRPVAARVRVGKQIHRGIDC	240
DB	181	PLGPEAQAASOGH	LTLELVLEGQVAAQSSVILGGAHRPVAARVRVGKQIHRGIDC	240
OY	241	QGSRRACQEPFVDR	ETIGMHWITIOPEGYAMNCIGQCPHLTAGMGIAASFHTAVLN	300
DB	241	QGSRRACQEPFVDR	ETIGMHWITIOPEGYAMNCIGQCPHLTAGMGIAASFHTAVLN	300
OY	301	LKANTAACTGGGSC	VPJARPLSLTYDRDSNVKTDIPDMVEAGCS	352

Db 301 LKANTAAGTTGGSCVPTRRRPLSLYYDRDSNIVKTDIPDMVEACGCS 352

RESULT 2

activin beta C mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 26-Aug-1999
 C:Accession: JCS366
 R:Pang, J.; Wang, S.; Smiley, E.; Bonadio, J.
 Biochem. Biophys. Res. Commun. 231, 655-661, 1997
 A:Title: Genes coding for mouse activin beta C and beta E are closely linked and exhibit
 A:Reference number: JCS366; MUID:97224404
 A:Accession: JCS366
 A:Molecule type: DNA
 A:Residues: 1-352 <FAM>
 A:Cross-references: GB:095962
 C:Comment: Activin beta C and beta E form a distinct subset of related activins.
 C:Genetics:
 A:Introns: 105/3
 C:Superfamily: inhibin

Query Match	75.6%	Score 1398	DB 2	Length 352
Best Local Similarity	76.2%	Pred. No. 3.1e-118		
Matches 269	Conservative 32	Mismatches 50	Indels 2	Gaps 2

QY	1	MTSLLALFLAPTTVNTPRAGOCRCACGPTILESOBELLDLAKRSILDKLHNTOR	60
Db	1	MASSLLALFLPTTVNPNTEGRCACWALFIDLESORELLDLAKRSILDKLHLSOR	60
QY	61	PTLRPVSBAALRTALOHILHVGPOGALLE-DINROECETIISEAFELGSLTINOTRLDHFHS	119
Db	61	PILSRPVSNGLAKTLAORLRGCRREPTLENDQROEYEIISPADULDSINOTRLIEFFHS	120
QY	120	SDRTACDREVQASLMEFVQLPSNTWTTLKVRVLVGLPHTNMLTLATQYLEEVDASGHW	179
Db	121	G-MSAGMGVETROTBMFEFVQCPRHNAQTMMIRVLRLPDTMLTLTSQVYVQVNASGHW	179
QY	180	LPLGSPAQASQSGHLLTELVEGOVQASSVILGGAAHHPFYAAHVRVVGKQRIHRRGID	239
Db	180	LLLGAPPAQASQGHLLTELVEPESOVHSSLIGMFSHRPFPAAOVVRREGKHHRRRGID	239
QY	240	CGGSGHMCROEFFPDRFEIEMHDMIIOPRGYAMNFCIOCGCLHTAIGMPRTIASFHTAYL	299
Db	240	CGGSGHMCROGEFVDPDRFEIOMHDMIIOPRGYAMNFCITQCCPLHVAQMPGISASFHTAYL	299
QY	300	NLLKANTAACTGGGSCCVPYARRPLSLTLYYDRDSNIYKTDIPDMVYACGCS	352
Db	300	NLLKANAAGAATTGRCSCCVPYSRRPLSLTLYYDRDSNIYKTDIPDMVYACGCS	352

RESULT 3

activin beta precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1995
 C:Accession: S70580
 R:Lau, A.L.: Nishimori, K.; Matzuk, M.M.
 Blochim. Biophys. Acta 1307, 145-148, 1996
 A:Title: Structural analysis of the mouse activin beta-C gene.
 A:Reference number: S70580; MUID:96283807
 A:Accession: S70580
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-352 <LAU>
 A:Cross-references: EMBL:U40772
 C:Genetics:
 A:Introns: 106/1
 C:Superfamily: Inhibdin

Query Match	75.38;	Score 1392;	DB 2;	Length 352;
Best Local Similarity	75.98;	Pred. No. 1.1e-117;		

Matches 268; Conservative 32; Mismatches 51; Indels 2; Gaps 2.

```

OY      1 MMSLLALALLAAPTVAATPRAGGCCPACGGPTLEESORELLDLAKRSILDKLHLTOR    60
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MASSLLALLALTPTTVAAPTEGSCPMCAIIDELESORELLDLAKKSILDKLHLSOR    60
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      61 PLINRPVSHAAURLTAQLQHLHGVPQCALLF-DNRDCEEIIISPAETGISTNORLDPFHS    119
          | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 PLSRPPVSGALKATMOLRLRGRRRETI LLEHQOREEEIISFAOTDISSINORLFPHS    120
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      120 SRTTGCDHEVQOASIMFFVOLPSNTMTLKLVLYLGAPHNTNLTLAYQLLEYEDASGMQ    179
          | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . |
Db      121 G-RMASGMEVRQTRMEFFVEQEPHNATQTMIRVLRYLPDYDTNLITLSQVYVGNASGMQ    179
          | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . |
OY      180 IPLGEAOAACSOGHTLETYLEGOVAOSSYLIGGAHRFPVAVARVARGKHDIRRGID    239
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      180 LLGLGEDAQAACSOGHTLETYLEPESOVASHSLILGWFSHPRPVAAQYRVBEKIHVRRGID    239
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      240 CGGSGRMCRCROEFDFPREIGHMWMITTOPSGYAMNFICGCPRIHMGIAASPIITAVAL    299
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      240 CGGASRMCCRQREFDYDRREIGHMNWMITTOPSGYAMNFICGCPRIHVAGMGISAPIITAVL    299
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      300 NLKANTAAGTTGGSCCVPARRRPLSLYYDRDSNVIVKTIDPDMAVEACGS    352
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      300 NLLKANAAAGTTGGSCCVPTSRRLPLLYYDRDSNVIVKTIDPDMAVEACGS    352
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT

A:activin beta D chain precursor - African clawed frog
C:Species: *Xenopus laevis* (African clawed frog)
C:Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
C:Accession: J04151
R:Oda, S.; Nishimatsu, S.; Murakami, K.; Ikeno, N.
Biochem. Biophys. Res. Commun. 210, 581-588, 1995
A:Title: Molecular cloning and functional analysis of a new activin beta subunit: a d
A:Reference number: J04151, MUID:95275314
A:Accession: J04151
A:Molecule type: mRNA
A:Residues: 1-367 <ODA>
A:Cross-references: DDBJ:ID49543; NID:9961512; PIDN:BA008494.1; PID:9961513
A:Experimental source: embryo
C:Superfamily: inhibin
C:Keywords: glycoprotein; mesoderm
F:1-253/Domain: signal sequence #status predicted <SIG>
F:254-367/Product: activin beta D chain #status predicted <MAT>
F:64,135,161,208,230/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match	37.28;	Score 688.5;	DB 2;	Length 367;
Best Local Similarity	40.48;	Pred. No. 3.3e-54;		
Matches 147;	Conservative 65;	Mismatches 125;	Indels 27;	Gaps 8.

```
0Y      5 LLAFLLLATPTTATPRAGOCPCACGGPPLLEBESORELLDLAKRSTLXKLTORPPLN 64
Db      15 LTLGALAASTQGLTKRS-----QQPSGC-----YODKEEVELKKOOLITKLHKERPNT 66
0Y      65 RPVSRAALRTALOHLH-GVPQCAL-----EDNRBOECETISPAETGSTINQ 11
|       | :   | :   | :   | :   | :   | :   | :   | :   | :   | :   | :   |
Db      67 HPVPRGAVAAVALRLRLHNKRMEGLEFGSNMDSMTENTDIDQSYELISFAET EYTENS 12
|       | :   | :   | :   | :   | :   | :   | :   | :   | :   | :   | :   |
0Y      112 TRLDFHSSDRTAGREVOAALMFVGYLPBSNTTWLAKVAVLVLGPHNMLTAFUYILE 17
|       | :   | :   | :   | :   | :   | :   | :   | :   | :   | :   | :   |
Db      127 ITLNFOOTTRKEO-SAHVIQAHLMLFFEAANTSOQNETHLYLVOEAYSRIILISEKLE 18
|       | :   | :   | :   | :   | :   | :   | :   | :   | :   | :   | :   |
0Y      172 VDASGHQOLPLFGEAOACASOGHLTELVLEIGVOASSYLIGA--ANRPVAARVRGCG 22
|       | :   | :   | :   | :   | :   | :   | :   | :   | :   | :   | :   |
Db      186 PRMGWQTESLSKMLOTFEFDGKNKSLOLELNCDCODVPYLANPNNSHOPLVAAQKVNE 24
|       | :   | :   | :   | :   | :   | :   | :   | :   | :   | :   | :   |
0Y      230 K-HQIHRRGIDCGSGSRRMOREFVDPRELJGDIMDTIOREGVAMNFICISOPRLTGMR 28
|       | :   | :   | :   | :   | :   | :   | :   | :   | :   | :   | :   |
Db      246 QSHIHATKSLINCDOANSNLCCRDYYVDPKDIGMDWTIKREGIQIYNWCGLCSPMHTIAAP 30
|       | :   | :   | :   | :   | :   | :   | :   | :   | :   | :   | :   |
0Y      289 GIASHFTIVAILDKANTRAAGTTGGSCCYPTARRPLSLLYDRDSNIKYTDIDPMVEA 34
```

Db 306 GMA5FHTVTLNLIKANNI--QTAVNSCVPTKRRPRLSMKLFPRNNNVKATDADIMVEA 363
 349 CGCS 352
 364 CGCS 367

RESULT 5

JC5241

activin beta E chain precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 25-Apr-1997 #sequence_revision 09-May-1997 #text_change 29-Oct-1999

C:Accession: JC5241; JC5367

R:Yang, J.; Yin, W.; Smiley, E.; Wang, S.Q.; Bonadio, J.

Biochem. Biophys. Res. Commun. 228, 669-674, 1996

A:Title: Molecular cloning of the mouse activin beta E subunit gene.

A:Reference number: JC5241; MUID:97096313

A:Contents: liver

A:Accession: JC5241

A:Molecule type: mRNA

A:Residues: 1-350 <FAN>

A:Cross-references: GB:096386; NID:g2072521; PIDN:AAB53801.1; PID:g2072522

R:Yang, J.; Wang, S.; Smiley, E.; Bonadio, J.

Biochem. Biophys. Res. Commun. 231, 655-661, 1997

A:Title: Genes coding for mouse activin beta C and beta E are closely linked and exhibit

A:Reference number: JC5366; MUID:97224404

A:Accession: JC5367

A:Molecule type: DNA

A:Residues: 1-350 <FA2>

A:Cross-references: GB:096386; NID:g2072521; PIDN:AAB53801.1; PID:g2072522

C:Genetics:

A:Introns: 99/3

C:Superfamily: Inhibin

Query Match 35.0%; Score 648; DB 2; Length 350;
 Best Local Similarity 42.4%; Pred. No. 1.4e-50;
 Matches 153; Conservative 58; Mismatches 118; Indels 32; Gaps 14;

QY 6 LAFLLAPTTVTPRAGGCGPRTLEESQRELLDLAKRSILDKHLTOPPTLR 65
 8 LMLLMLALWVQSRSA--CPGCGPTLAPGQERALVLELKKOILLEGHLTSRPTTR 65
 QY 66 PSRAALRTALQHLGVPQALLEDNRQECETISFA--ETGLSTINOTRIIDFFSSDR 122
 66 PLFOALITRALRLQ--PK-SWPGNR--KVISPAITIDKSTSY--RSMJLPQLS--- 115
 Db 123 TAGDREVQASLMFVQVLPSTNTTLKRVLYLGPHTNLTATYLF--VDASGMHQL 180
 116 PLMSHHLHYHARL--WLHVPPSPGTLYLRIFRG--TTRCRGRFRFLAEHQTTSGMHAL 171
 QY 181 PLCPENQAACSGHLELLEGVQVQSS-----VILGGA-HRPFVAVRVG--GKH 231
 172 TLPSGGRSDSGVVKQLLEFRPLDLNSTAGLPRLLDLTACGQRFLELKRANPEAG 231
 Db 232 QIHRGIDCGGSRMCCROEFVDFREIGWHDWIIQPEGVANMFCIGQCLHIAAGPIA 291
 232 RARRRTTCERPTLCRRHYYDFQELGWRDWILOPEGYOLNYCSGQCPPLHLAGSPGIA 291
 QY 292 ASPTAVLNLKANTAACTGGSCCPTARRRLSLLYDRDSNLYKTIIPMNVYACCC 351
 292 ASFHSAVSLKANNP--WPAGSSCCVPTARRRLSLLYLDHNGNVKTVDPKVVAEACGC 349
 Db 352 S 352
 350 S 350

RESULT 6

151199

activin beta B subunit - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999

C:Accession: 151199
 R.Dohmann, C.E.; Hemmati-Brivanlou, A.; Thomsen, G.H.; Fields, A.; Woolf, T.M.; Melt
 Dev. Biol. 157, 474-483, 1993

A:Title: Expression of activin mRNA during early development in *Xenopus laevis*.

A:Reference number: 151199; MUID:93273083

A:Accession: 151199

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-370 <DOH>

A:Cross-references: GB:S61773; NID:g386027; PIDN:AAB26863.1; PID:g386028

C:Superfamily: Inhibin

Query Match 32.9%; Score 607.5; DB 2; Length 370;
 Best Local Similarity 36.6%; Pred. No. 6.7e-47;
 Matches 140; Conservative 70; Mismatches 122; Indels 51; Gaps 14;

QY 5 LILAPLL--LATTATATRAGGCGPRTLEESQRELLDLAKRSILDKHLTOPPT 62
 4 LILPLLAGLACAPSPPERGCPSC--HPMEPE-----MLEAVKRHLITLHMDRPN 57
 Db 63 LRRPVSRALRTALQHLGVPQALLED-----NRQECETISFAET 104
 58 ITHNVRAAMVSAALKRIA--GRVREDGNLEIPDLGHSLPFGHSHENSAREITPAET 114
 QY 105 GLSTINQTRLDHFSSDRTAGDRE--VQASLMFVQVLP---SMTWTLLKRVLYLGP 159
 115 DVDTASRVSLFTIANE--GNQNLVFOSLMLYLKLPYWDKSRRIKRVHFDAPN 171
 QY 160 TNLTLATQYLFLEVDASGMHQLPGEAQAACSG--HTLELVLEGQVQSSV-----L 212
 172 PDMNNVKKVDLRSGWHTFPLTAIOSLPEEGRRRLNLEVQCDG--CGESVLPYVDP 230
 Db 213 GGAHRPFVAAARVVG--GKHQIHRGIDCGGSRMCCROEFVDFREIGWHDWIIQPEGY 271
 231 GEESHRLPLVHARLADNKRIRKRGLECDGHTNLCCROFYIDRLGMDWIIAPAGY 290
 QY 272 AMNFCIGQCPRLHAGPGLAASFHTAVNLKANTAACTGG--GSCCVPARRRPLSLY 329
 291 YGVNCEGSCPAYLAGVGGASSFHTAVNQMRYMR--GLNPQTVNSCCTPKLSTMSMLY 347
 QY 330 YDRDSNIVKTDIPDMVVEACCS 352
 348 FDEYNIVKRDVNMIVDECGCA 370
 Db

RESULT 7

S50899

betab inhibin precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999

C:Accession: S50899

R:Thompson, D.A.; Cronin, C.N.; Martin, F.

Eur. J. Biochem. 226, 751-764, 1994

A:Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and bet

A:Reference number: S50897; MUID:95112839

A:Reference number: S50897; MUID:95112839

A:Accession: S50899

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-408 <THO>

A:Cross-references: EMBL:016240

C:Genetics:

A:Introns: 151/1

C:Superfamily: Inhibin

Query Match 32.7%; Score 605; DB 2; Length 408;
 Best Local Similarity 36.6%; Pred. No. 1.3e-46;
 Matches 145; Conservative 62; Mismatches 117; Indels 72; Gaps 15;

QY 13 APTTAVTPRA-----GQ--CPAGCGPTLEESQREL-----LIDLAKRSIL 52
 29 SPTRPPLPAPAPQPPPPGAGSGQDTCSCG-----FRPEELAGVDDDFLEAVNRHL 84
 Db

QY 53 DKHLTORPTLNRPVSRALFTALQHLGVPQALLEDNR-----EQE 95
 Db 85 NKLQKRGKRNTHAVPKAMATLAKLHA---GKVRDEGRVEIPLDGHASPGADGQERY 141
 QY 96 CEIISFAETGLSTINOTLDFHFSDDRTAGDRE--VOQASIMFPVOLPSMTWTTL----- 148
 Db 142 SEIISFAETGLDGLASSRVLRYEFSISNE--GNQLFVVQASIMLYLKL--LPVYLEKGR 195
 QY 149 -KVRVLVLPNH--TNLTLATQVLEVDASGMHQLPLGPEQAACSGHLELVLEGY 205
 Db 196 KVRVRYVVGQEGDPCDRAAVEKRVDLKRSQMTFFPLTEPIQLFSGERRSLDVOQDS 255
 QY 206 AOSVYL-----GGAHRRPFVAARVRV-GKHQIHRRGIDCGGSRMCCROEFVDFRE 258
 Db 256 CRELAIVVFPVDPGEESHRRPFVVQARLGDSRRIRKRGLECDGRTNLCROQPFIDFRL 315
 QY 259 IGMHDMITIOPEGYAMNFCIGCPHLIAGMGIASFTVAVNLKANTAACTGG--GSC 316
 Db 316 IGMNDMITIAPTYGYNCEGSCPAYLAGVPGSASSFTAVVQYRMR--GLNPQTVNSC 372
 QY 317 CVPTARRPLSLYYDRDSNIVKTDIPDMVVEACGCS 352
 Db 373 CIPTKLSTMSMLYFDDEYNIVKRDVPMIIVEEGCA 408

RESULT 8

A40150
 Inhibin beta-B chain precursor - human

N:Alternate names: activin AB chain B
 C:Species: Homo sapiens (man)
 C>Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text_change 01-Dec-2000

A:Accession: A40150; C24248; A40156; S10751
 R:Masou, A.J.; Berckemeler, L.M.; Schmelzer, C.H.; Schwall, R.H.
 Mol. Endocrinol. 3, 1352-1358, 1989

A:Title: Activin B: precursor sequences, genomic structure and in vitro activities.
 A:Reference number: A40150; MUID:90114200
 A:Accession: A40150

A:Molecule type: DNA
 A:Residues: 1-407 <MAS>

A:Cross-references: GB:M31668; GB:M31669; NID:g186419; PIDN:AAA59451.1; PID:g386827
 R:Masou, A.J.; Niall, H.D.; Seeburg, P.H.
 Biochem. Biophys. Res. Commun. 135, 957-964, 1986

A:Title: Structure of two human ovarian inhibins.
 A:Reference number: A90123; MUID:86186863

A:Molecule type: mRNA
 A:Residues: 55-407 <MA>
 A:Cross-references: GB:M13437; NID:g186416; PIDN:AAA59169.1; PID:g186417

R:Feng, Z.M.; Bardin, C.W.; Chen, C.L.C.
 Mol. Endocrinol. 3, 939-948, 1989
 A:Title: Characterization and regulation of testicular inhibin beta-subunit mRNA.
 A:Reference number: A40156; MUID:89295443

A:Accession: A40156
 A:Molecule type: mRNA

A:Residues: 22-46, 'A', 48-407 <FEN>
 A:Cross-references: GB:M31632

R:Schmelzer, C.H.; Burton, L.E.; Tamony, C.M.; Schwall, R.H.; Masou, A.J.; Liegeois, N.
 Blochim. Biophys. Acta 1039, 135-141, 1990
 A:Title: Purification and characterization of recombinant human activin B.
 A:Reference number: S10751; MUID:90304183

A:Accession: S10751
 A:Molecule type: protein

A:Residues: 293-294, 'GX', 297-302, 'XX', 305-307 <SCH>
 C:Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respectively.

C:Genetics:
 A:Gene: GDB:INHBB

A:Cross-references: GDB:119347; OMIM:147390
 A:Map position: 2cen-2q13
 C:Superfamily: Inhibin

C:Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone
 F:1-207Domain: signal sequence #status predicted <SIG>

F:21-292/Domain: propeptide #status predicted <PRO>
 F:293/Product: Inhibin beta-B chain #status predicted <MA>
 F:93/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 32.4%; Score 599.5; DB 1; Length 407;
 Best Local Similarity 36.6%; Pred. No. 46-46;
 Matches 145; Conservative 60; Mismatches 118; Indels 73; Gaps 16;

QY 13 APTVATPRA-----GGQ---CPACGPTLESGREL-----LIDAKRSIID 53
 Db 29 SPTPEPTAAPPPPPGSGSDTCTSCG---PRREEGRDGDPLEVAKHILS 84
 QY 54 KLHLTORPTLNRPVSRALFTALQHLGVPQALLEDNR-----EDEC 96
 Db 85 RLQMRGRNTHAVPKAMATLAKLHA---GKVRDEGRVEIPLDGHASPGADGQERY 141
 QY 97 EIIISFAETGLSTINOTLDFHFSDDRTAGDRE--VOQASIMFPVOLPSMTWTTL----- 148
 Db 142 SEIISFAETGLDGLASSRVLRYEFSISNE--GNQLFVVQASIMLYLKL--LPVYLEKGR 195
 QY 149 KVRVLVLP--GPHNTNLTLATQVLEVDASGMHQLPLGPEQAACSGHLELVLEGY 205
 Db 196 KVRVRYVVGQEGDPCDRAAVEKRVDLKRSQMTFFPLTEPIQLFSGERRSLDVOQDS 254
 QY 206 AOSVYL-----GGAHRRPFVAARVRV-GKHQIHRRGIDCGGSRMCCROEFVDFRE 258
 Db 256 CRELAIVVFPVDPGEESHRRPFVVQARLGDSRRIRKRGLECDGRTNLCROQPFIDFRL 314
 QY 259 IGMHDMITIOPEGYAMNFCIGCPHLIAGMGIASFTVAVNLKANTAACTGG--GSC 316
 Db 315 IGMNDMITIAPTYGYNCEGSCPAYLAGVPGSASSFTAVVQYRMR--GLNPQTVNSC 371
 QY 317 CVPTARRPLSLYYDRDSNIVKTDIPDMVVEACGCS 352
 Db 372 CIPTKLSTMSMLYFDDEYNIVKRDVPMIIVEEGCA 407

RESULT 9

B41398

Inhibin beta-B chain precursor - rat

N:Alternate names: inhibin/activin beta B-chain
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 03-Apr-1992 #sequence, revision 01-Aug-1997 #text_change 16-Jul-1999

A:Accession: B41398; I53288; C40905
 R:Feng, Z.M.; Li, Y.P.; Chen, C.L.C.
 Mol. Endocrinol. 3, 1914-1925, 1989

A:Title: Analysis of the 5'-flanking regions of rat inhibin alpha- and beta-B-subunit
 A:Reference number: A41398; MUID:90190649
 A:Accession: B41398

A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-174 <FEN>
 A:Cross-references: GB:M32756; GB:M32757; NID:g204943; PIDN:AAA41438.1; PID:g554460

R:Dykema, J.C.; Mayo, K.E.
 Endocrinology 135, 702-711, 1994
 A:Title: Two messenger ribonucleic acids encoding the common beta B-chain of inhibin
 A:Reference number: I53288; MUID:94307180

A:Accession: I53288
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-7 <RES>

A:Cross-references: GB:S72477; NID:g619268
 R:Esch, F.S.; Shimazaki, S.; Cooksey, K.; Mercado, M.; Masou, A.J.; Ying, S.Y.; Ueno,
 Mol. Endocrinol. 1, 388-396, 1987

A:Title: Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence analysis
 A:Reference number: A40905; MUID:90331931
 A:Accession: C40905

A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 133-411 <ESC>

C:Superfamily: Inhibin

Query Match 32.2%; Score 595.5; DB 2; Length 411;


```

Best Local Similarity 35.5%: Pred. No. 9,4e+6;
Matches 139; Conservative 65; Mismatches 127; Indels 61; Gaps 12.

QY      13 APTTVATPRA-----GQC---CPACGGPTLEESQEL-----LDDAKSIID 53
           :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db      29 SPTRPPSPAPRPPPPPGARCGSODTCTSCGGGGGFRRPELRGVDDLEAVKRIILS 88
QY      54 KLHLTOPFLNRVSRALRTALQLHLCVPALLIEDNR-----EDEC 96
           :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db      89 RLQGRPNNTIHAHPAAWYTLARKLHA---GKVEDDERVEIPHLDGHASBGADGGERVS 145
           :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
QY      97 EISFAETGLSTINORLDHFESSDETACDRE--VQAQSIMLFVQ----LPSTNTWLTK 149
           |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db     146 EISFAETDLGLASSRKLIFFVSN---GNQLMFVQAQSIMLKLPYLVEKSSRRKR 202
           |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY     150 VRVVLDPHTNLTLLATQYLEVDVASGMWOLPLGPBAQACSQGHLELVLEGVAQSS 209
           :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db     203 VKYVFQOGHGIDRNRYVEKKVLDLRKSGMHTFPIETAIALFERGERRLINDLYDCSQDEL 262
QY     210 VIL-----GGAHRPRPVAAKRVVG-GKQIOIRRGIDCOGSRMCCREFVADREIGWH 262
           :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db     263 AVPEVFDPCGEHSRPVVVQAQLRGDSRHRIKRGECGRSLCLCCROQFIIDLRLGWN 322
QY     263 DMIIQPBEYAMNFPIQGCRPHLAGMGIAASFHTVNLTKANTAAQTGG--SCSCPVT 320
           |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db     323 DMIITPCTGYENYEGSCPAYLAVGPSASSFTTAVANQYRR--GLNPQVNSCRIPT 379
QY     321 ARRLPSLLTYGRDSNIYKTIDIPMVNAAGCS 352
           :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db     380 KLSMSMLTFDEDEYNIVKRDVPKNMIVECCCA 411
```

```

RESULT 10
MFGGB
Inhibin beta-B chain precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 01-Dec-2000
C:Accession: A01394
R:Masou, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Guillemin, R.;
Nature 318, 659-663, 1985
A:Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precursor
A:Reference number: A93371; MUID:86092207
A:Accession: A01394
A:Molecule type: mRNA
A:Residues: 1-349 <MAS>
A:Cross-references: GB:X03267; NID:92005; PIDN:CAA27021.1; PID:92006
C:Comment: The source of this protein is ovarian follicular fluid.
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide.
I:Ident forms of Inhibin have been isolated (A and B) that differ in the amino-terminal
C:Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of follitropin
C:Superfamily: Inhibin
K:Keywords: contraceptive; follitropin inhibitor; glycoprotein; gonad
F:-23/-Domain: propeptide (fragment) #status predicted <PRO>
F:235-349/Product: Inhibin beta-B chain #status predicted <MA>
F:35/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          31.7%; Score 587; DB 1; Length 349;
Best Local Similarity 37.7%; Pred. No. 4, 4e-45;
Matches 129; Conservative 62; Mismatches 109; Indels 42; Gaps 9;

Oy   44 LDLAKSILDKLHLTORPTLNRPVSRALFTALQHLHGVPQCALLEDNR----- 92
      ||| | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db   17 LEAVKRHLRLNLRMGCRPNITTHAVPKRAAMATARKLHA--GKVREDGRVEIPIHLDGNAS 73
      ||| | | | : | : | : | : | : | : | : | : | : | : | : | : |

Oy   93 -----QDECELIISFEATGLSTINOTRLDFPFSDDTRAGRE--VOOASLMFPVQ----- 139
      ||| | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db   74 PGADGGRVESLIISFEATDGLASSRVNLFFISIE---GMQNLFVVQASIMLYLKLLPVY 130
      ||| | | | : | : | : | : | : | : | : | : | : | : | : | : |

Oy   140 LPSMTTTLTKRVYLVLPHNTNLTLATQYLEVDASGMOLPLGPFAOAACSGHLTLEI 199
      ||| | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db   131 LEKSRRRKVRKRVYFOEPBGHDMDVYEKRVDLKRSQWMLLPTEIAIALFERGERRLNI 190
      ||| | | | : | : | : | : | : | : | : | : | : | : | : | : |

Oy   200 VLEGQVAOSSVIL-----GGAAHRPFVAVARNVG-GKHDIHKRGIDCGGSMMCCRQEF 252

```

Db 191 DVCCDCCGCLAVVAPVFDVPDGESHRRPVVQVAVQALGDSRRIRIKKRLBEDDGTNLCNCNQOF 250

Qy 253 FVDREIRIGHMDIIOPEGYAMNFCIGCCPLHIAGMPTIASHTFVNLNLKANTAACTTG 312

Db 251 FIDFRLIGKSDMIAPTYGYNYCEGSCPAVLGAVGSASSHPTVVVNOYBMR--GLNP 307

Qy 313 G--GSCVPTARRPLSLLLYYRDSNIWKTPIPMVAVCAAGCS 352

Db 308 GYVNSCCIPFKLSTYMSMLTFPDEYNIVYKRDVPMHIVEECGCA 349

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RESULT 11
150103
activin beta B - zebra fish
C:Species: Brachydanio rerio (zebra fish)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: 150103
R:Wiltbrodt, J.; Rosa, F. M.
Genes Dev. 8, 1448-1462, 1994
A:Title: Disruption of mesoderm and axis formation in fish by ectopic expression of a
A:Reference number: 150103; MUID:95011555
A:Accession: 150103
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-393 <NIT>
A:Cross-references: EMBL:X76051; NID:g516356; P1DN:CAAC53636.1; P1D:g516357
C:Genetics:
A:Gene: Zactbetab
C:Superfamily: Inhibin

```

[illegible]

RESULT 12
MPCGBA
Inhibin beta-A chain precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 13-Aug-1986 #sequence=reviston 13-Aug-1986 #text_change 18-Jun-1999
C:Accession: A01993
R:Meson, A.J.: Haylick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Gullilemin, R.
Nature 318, 659-663, 1985
A:Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precursors

A:Reference number: A9371; MUID:86092207
 A:Accession: A01393
 A:Molecule type: mRNA
 A:Residues: 1-424 <MAS>
 A:Cross-references: GB:X03266; NID:92002; PIDN:CAA27020.1; PID:92003
 C:Comment: The source of this protein is ovarian follicular fluid.
 C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide.
 C:Comment: Inhibin have been isolated (A and B) that differ in the amino-terminal
 C:Superfamily: Inhibin
 C:Keywords: contraceptive; follicle-inhibitor; glycoprotein; gonad
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-308/Domain: propeptide #status predicted <PRO>
 F:309-424/Product: Inhibin beta-A chain #status predicted <MAT>
 F:165/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 30.4%; Score 562; DB 1; Length 424;
 Best Local Similarity 31.2%; Pred. No. 1e-42;
 Matches 131; Conservative 69; Mismatches 142; Indels 78; Gaps 10;

QY 6 LLAFLLLAPTVATPRAG-----QPCAGGPTL--ELESGRELLDLAKRSILDKLHLT 58
 DB 10 LLAFLLLAPTVATPRAG-----QPCAGGPTL--ELESGRELLDLAKRSILDKLHLT 58
 QY 59 ORPTLNRPVSRAALRTALQHLH-----GVPGALLDNRQCEETISPAET 104
 DB 70 KRPDVTPVPKALMLNIRKLHVKGKGVNGEYLEDIDGRRAEMNEIMQETSEITFAEA 129
 QY 105 GLSTINOTRLDFHPSDRTAGDRE-VQASLMFPVOLP-SNTTWL-LKRVYLGLPH-- 156
 DB 130 GTA-----RKTLEFSEIKESGSDLSVERAEVLFKVPKANKRTTRVSLRLEQOORRPOG 184
 QY 157 -----PHNNTLTAQYLLLEVDASGMHQLPLGPEAQ-----AAC 190
 DB 185 SADAGEAEVDGFEERSEVLISEKVVDAKSTWHTFPVSSIORLLDQKSLADIRAC 244
 QY 191 SOGHLT-LELYEGVAVOSSVYLQ-----AAHRRPVAAVRVGGK--HQ 232
 DB 245 ECHETGASLVLLGKKKKKEEAEGRKROEGAGVDEKEQSHRPLMLQAROSEHPHR 304
 QY 233 IHRGIDCGGSMCCROEFVDFREIGMHWIIOPEGYAMNFCIGCPHLIAGMPGIA 292
 DB 305 RRRRGLECDCKVNICCKKOFVSKDIGMNDWITAPSGHANYCEGESHLAGSGSL 364
 QY 293 SFHFAVLNLLKANTAGTGGSCVPTARRPLSLIYDRDSNYKTDIPDMVVEACGC 352
 DB 365 SFHSTVINYHBMGHSFPANLKSCVPTKLRPMISMLYDDGONITIKDIONNIVECGCS 424

RESULT 13

S31440

Inhibin beta-A chain - mouse

N:Alternate names: activin A; mesoderm-inducing factor WEHI-MIF
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999
 C:Accession: A60087; 148265; S31440

R:Albano, R.M.; Groome, N.; Smith, J.C.
 Development 117, 711-723, 1993
 A:Title: Activins are expressed in preimplantation mouse embryos and in ES and EC cells

A:Reference number: 148243; MUID:9321614
 A:Accession: 148265
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-424 <RES>
 A:Cross-references: EMBL:X69619; NID:950145; PIDN:CAA49325.1; PID:950146

C:Superfamily: Inhibin

Query Match 30.2%; Score 559; DB 1; Length 424;
 Best Local Similarity 32.1%; Pred. No. 1.9e-42;
 Matches 135; Conservative 71; Mismatches 135; Indels 80; Gaps 12;

QY 6 LLAFLLLAPTVATPRAG-----QPCAGGPTLELE--SORELLDLAKRSILDKLHL 57
 DB 10 LLAFLLLAPTVATPRAG-----QPCAGGPTLELE--SORELLDLAKRSILDKLHL 57
 QY 58 TORPLNRPVSRAALRTALQHLH-----GVPGALLDNRQCEETISPAE 103
 DB 69 KRPDVTPVPKALMLNIRKLHVKGKGVNGEYLEDIDGRRAEMNEIMQETSEITFAEA 128
 QY 104 GLSTINOTRLDFHPSDRTAGDRE-VQASLMFPVOLP-SNTTWL-LKRVYLGLPH-- 158
 DB 129 SGT-----RKTLEFSEIKESGSDLSVERAEVLFKVPKANKRTTRVSLRLEQOORRPOG 183
 QY 159 -----PHNNTLTAQYLLLEVDASGMHQLPLGPEAQ-----AAC 190
 DB 184 SADAGEAEVDGFEERSEVLISEKVVDAKSTWHTFPVSSIORLLDQKSLADIRAC 244
 QY 203 GOVAQSS-----VILG-----GAHRRPV--VAARVVGKH 231
 DB 244 ECHETGASLVLLGKKKKKEEAEGRKROEGAGVDEKEQSHRPLMLQAROSEHPHR 303
 QY 232 IHRGIDCGGSMCCROEFVDFREIGMHWIIOPEGYAMNFCIGCPHLIAGMPGIA 291
 DB 304 RRRRGLECDCKVNICCKKOFVSKDIGMNDWITAPSGHANYCEGESHLAGSGSL 363
 QY 292 SFHFAVLNLLKANTAGTGGSCVPTARRPLSLIYDRDSNYKTDIPDMVVEACGC 351
 DB 364 SFHSTVINYHBMGHSFPANLKSCVPTKLRPMISMLYDDGONITIKDIONNIVECGC 423
 QY 352 S 352
 DB 424 S 424

RESULT 14

B24248

Inhibin beta-A chain precursor (validated) - human

N:Alternate names: activin A; activin AB chain A; erythroid differentiation factor; m
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 08-Dec-2000
 C:Accession: S30488; B24248; A30884; S33551; P00010

R:Uemoto, K.; Handa, S.I.; Ueno, N.; Murakami, K.; Fukumizu, A.
 DNA Seq. 2, 103-110, 1991

A:Title: Structure and sequence analysis of the human activin beta(A) subunit gene.
 A:Reference number: S30488; MUID:9213588

A:Accession: S30488
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-426 <TRAN>
 A:Cross-references: EMBL:X57578; NID:928351; PIDN:CAA40805.1; PID:9825621

A:Note: The authors translated the codon GAG for residue 53 as Gly and GAG for residu
 R:Stewart, A.G.; Milbortow, H.M.; Ring, J.M.; Crowther, C.E.; Forage, R.G.
 FEBS Lett. 206, 329-334, 1986

A:Title: Human inhibin genes. Genomic characterisation and sequencing.
 A:Reference number: A91366; MUID:87005283

A:Accession: B24248
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 311-426 <STE>
 A:Cross-references: GB:X04447; NID:933928; PIDN:CAA28041.1; PID:933929

R:Wason, A.J.; Niall, H.D.; Seeburg, P.H.
 Biochem. Biophys. Res. Commun. 135, 957-964, 1986

A:Title: Structure of two human ovarian inhibins.
 A:Reference number: A90123; MUID:86186863

A:Accession: B24248
 A:Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-426 <MAS>
 A:Cross-references: GB:M13436; NID:9186414; PIDN:AAA59168.1; PID:9307069

R:Murata, M.; Eto, Y.; Shibata, H.; Sekai, M.; Muramatsu, M.
 Proc. Natl. Acad. Sci. U.S.A. 85, 2434-2438, 1988

A:Title: Erythroid differentiation factor is encoded by the same mRNA as that of the Inh
 A:Reference number: A30884; MUID:86190086
 A:Accession: A30884
 A:Molecule type: mRNA
 A:Residues: 1-426 <MUR>
 A:Cross-references: GB:J03634; NID:q181946; PID:AAA35787.1; PID:q181947
 R:Berger, H.; Walter, M.; Northmann, W.
 Submitted to the EMBL Data Library, April 1993
 A:Description: Nucleotide sequence coding for the mature subunit beta(A) of human inhibi
 A:Reference number: S33351
 A:Accession: S33351
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 311-376, 'AC', 380-426 <BER>
 A:Cross-references: EMBL:X72498; NID:q297786; PID:CA51163.1; PID:q755740
 R:Fujimoto, K.; Kawakita, M.; Kato, K.; Yonemura, Y.; Masuda, T.; Matsuzaki, H.; Hirose,
 Blochem. Biophys. Res. Commun. 174, 1163-1168, 1991
 A:Title: Purification of megakaryocyte differentiation activity from a human fibrous hist
 A:Reference number: P00010; MUID:91144591
 A:Accession: P00010
 A:Molecule type: protein
 A:Residues: 311-313, 'X', 315-320, 'XX', 323-328, 'X', 330-334 <FUD>
 C:Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respecti
 bin beta-A and beta-B, respectively.
 C:Genetics:
 A:Gene: GDB:INHBA
 A:Cross-references: GDB:119346; OMIM:147290
 A:Map position: 7p15-7p13
 A:Introns: 129/3
 C:Superfamily: Inhibin
 C:Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone
 F:1-28/Domain: signal sequence #status predicted <SUG>
 F:29-310/Domain: propeptide #status predicted <PRO>
 F:311-426/Product: inhibin beta A chain #status experimental <MAT>
 F:165/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 30.1%; Score 557; DB 1; Length 426;
 Best Local Similarity 31.5%; Pred. No. 2,9e-42;
 Matches 133; Conservative 74; Mismatches 135; Indels 80; Gaps 12;

```

QY 6 LLAFLAAPTVAATPRAG-----QCPACGGPTL--ELSESORELLDLAKRSLDKLHLT 58
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 10 LLAFCWIIIVSSPTPGSEGHSAAPDCPSALALPKDVPNSQPEMEVAVKHILNMLHLK 69
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
QY 59 QRPFLNRPVSAALRTALQHL-----GVPGALLLEDNRDECEIISFAET 104
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 70 KRPTQTPVPRAALNLAIRKLHVKGKGENGYVEIEDIGRAEMNEMLEQTSIIITFAES 129
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
QY 105 GLSTINOTRLDPHFSSDRTAGDRE--VOOASLMFVOLP--SNTWT--LKVRVLVGLPH--- 158
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 130 GTA-----RKLHFEISKEGSDLSVERAEVWLFLKVPKANRRTKVTITLFGQCKHPG 184
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
QY 159 -----NTNLTATQYLLEVDASGWHQPLRPEAOACSGCHLTLEVLDS 203
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 185 SLDTGEAEAEVGLKKESEKELLSEKVVDAKRSKTHVPPVSSSIQRLDDQKSLDIRIAC 244
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
QY 204 QVAQSS---VILG-----GA-----AHRPF--VAARVRVGGK 230
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 245 EOCQSSGASLVLLKKKKKEEGEGKKKGGEGAGAGADEKEDSHRFLMLQAROSEDPH 304
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
QY 231 HQHRRGIDCGGSGMCCROEFVDFREIGHNMIIOPEGYAMFCTIGCQPLIAGMPGT 290
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 305 HRRRRTGLECDQKVNICKQKQFVSKDIGNDWIIPSGHNANYCEGECPSHLAGTSGS 364
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
QY 291 AASPTTAVLNLKANTAGTTCGSCCVPTARPLSLIYYDRDSNIYKTQIDPQWVEAG 350
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 365 SLTFSSTVNIHYRMGRGHPFANLASCVPFLKRPMSMLTYDGGONITKKIDQNIIVECG 424
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
QY 351 CS 352
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 425 CS 426
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :

```

RESULT 15

S50898

Inhibin beta-A chain precursor - bovine

N/Alternate names: activin; mesoderm inducing factor

C/Species: Bos primigenius laurus (cattle)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text-change 10-Sep-1999

C/Accession: S50898; B25732; A60960; B61548

R:Thompson, D.A.; Cronin, C.N.; Martin, F.

Eur. J. Biochem. 226, 751-764, 1994

A:Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and bet

y DNase I footprinting.

A:Reference number: S50897; MUID:95112839

A:Accession: S50898

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-425 <THO>

A:Cross-references: EMBL:U16238

R:Forage, R.G.; Ring, J.M.; Brown, R.W.; McInerney, B.V.; Cobon, G.S.; Gregson, R.P.;

Proc. Natl. Acad. Sci. U.S.A. 83, 3091-3095, 1986

A:Title: Cloning and sequence analysis of cDNA species coding for the two subunits of

A:Reference number: A94097; MUID:86205842

A:Accession: B25732

A:Molecule type: mRNA

A:Residues: 258-425 <FOR>

A:Cross-references: GB:M1274; NID:q163196; PID:AAA97415.1; PID:q163197

A:Note: part of this sequence, including the amino end of the mature protein, was con

R:Chertov, O.Y.; Krasnosel'skii, A.L.; Bogdanov, M.E.; Hopenkaya, O.A.

Biomed. Sci. 1, 499-506, 1990

A:Title: Mesoderm-inducing factor from bovine amniotic fluid: purification and N-term

A:Reference number: A60960; MUID:92126853

A:Accession: A60960

A:Molecule type: protein

A:Residues: 310-312, 'X', 314-319, 'XX', 322-328, 'P' <CHE>

R:Fukuda, M.; Miyamoto, K.; Hasegawa, Y.; Nomura, M.; Igarashi, M.; Kangawa, K.; Mats

Mol. Cell. Endocrinol. 44, 55-60, 1986

A:Title: Isolation of bovine follicular fluid inhibin of about 32 kDa.

A:Reference number: A61548; MUID:86136599

A:Accession: B61548

A:Molecule type: protein

A:Residues: 310-313 <FUK>

C:Genetics:
 A:Introns: 130/1

C:Superfamily: Inhibin

C:Keywords: disulfide bond; glycoprotein; gonad; heterodimer; homodimer; hormone

F:1-28/Domain: signal sequence #status predicted <SUG>

F:29-309/Domain: propeptide #status predicted <PRO>

F:310-425/Product: beta-A inhibin/activin #status experimental <MAT>

F:165/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 30.1%; Score 556.5; DB 1; Length 425;
 Best Local Similarity 31.1%; Pred. No. 3.2e-42;
 Matches 131; Conservative 76; Mismatches 135; Indels 79; Gaps 11;

```

QY 6 LLAFLAAPTVAATPRAG-----QCPACGGPTL--ELSESORELLDLAKRSLDKLHLT 58
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 10 LLAFCWIIIVSSPTPGSEGHSAAPDCPSALALPKDVPNSQPEMEVAVKHILNMLHLK 69
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
QY 59 QRPFLNRPVSAALRTALQHL-----GVPGALLLEDNRDECEIISFAET 104
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 70 KRPTQTPVPRAALNLAIRKLHVKGKGENGYVEIEDIGRAEMNEMLEQTSIIITFAES 129
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
QY 105 GLSTINOTRLDPHFSSDRTAGDRE--VOOASLMFVOLP--SNTWT--LKVRVLVGLPH--- 158
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 130 GTA-----RKLHFEISKEGSDLSVERAEVWLFLKVPKANRRTKVTITLFGQCKHPG 184
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
QY 159 -----NTNLTATQYLLEVDASGWHQPLRPEAOACSGCHLTLEVLDS 203
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 185 SLDTGEAEAEVGLKKESEKELLSEKVVDAKRSKTHVPPVSSSIQRLDDQKSLDIRIAC 244
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
QY 204 QVAQ---SSVIL-----GA-----AHRPF--VAARVRVGGK 231
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 245 EOCQSSGASLVLLKKKKKEEGEGKKRDEGAGAGDEKEDSHRFLMLQAROSEDPH 304
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
QY 204 QVAQ---SSVIL-----GA-----AHRPF--VAARVRVGGK 231
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
DB 245 EOCQSSGASLVLLKKKKKEEGEGKKRDEGAGAGDEKEDSHRFLMLQAROSEDPH 304
   |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :

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Tue Oct 15 13:49:40 2002

us-09-684-383-2.rpr

Page 8

Oy	232 QIHRRGIDCGGSRMCQREFPVORFREGHMDNITIOPEGYAMNFCTGGCPPLHIAQMPIA	291
Db	305 RRRRGLCEDGAKYNICKCKKPPYFKDIGNMNDIIASGHIANVCEGPCPSHAGTSGSS	364
Oy	292 ASFTFVLNLKANPAAGTTGGSCCPTJARPRLSLTYDRDSNTVKTDIPDYVEACGC	351
Db	365 LSHSTIVINIRGRGSHPANLASCVPATKLRPMSMLYYDDGONIKRKDIOMNIVEECGC	424
Oy	352 S 352	
Db	425 S 425	

Search completed: October 12, 2002, 02:09:55
Job time : 29 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 22:35:53 ; Search time 13.5 Seconds
(without alignments)
1009.576 Million cell updates/sec

Title: US-09-684-383-2

Perfect score: 1848
Sequence: 1 MTSSLLAFLLAPTTVATP.....DSNIVKTDIPDMVEACGCS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1849	100.0	352	1	IHBC_HUMAN
2	1392	75.3	352	1	IHBC_MOUSE
3	1379.5	74.6	351	1	IHBC_RAT
4	664	35.9	350	1	IHBE_HUMAN
5	648	35.0	350	1	IHBE_MOUSE
6	647	35.0	350	1	IHBE_RAT
7	605	32.7	408	1	IHBB_BOVIN
8	599.5	32.4	407	1	IHBB_HUMAN
9	598	32.3	391	1	IHBB_CHICK
10	587	31.7	349	1	IHBA_PIG
11	562	30.4	424	1	IHBA_RAT
12	561	30.3	424	1	IHBA_MOUSE
13	560	30.3	426	1	IHBA_HORSE
14	559	30.2	424	1	IHBA_MOUSE
15	557	30.1	426	1	IHBA_HUMAN
16	556.5	30.1	425	1	IHBA_BOVIN
17	552.5	29.9	425	1	IHBA_SHEEP
18	527	28.5	424	1	IHBA_CHICK
19	476	25.7	255	1	IHBA_MOUSE
20	305.5	16.5	405	1	GFPE_MOUSE
21	304.5	16.5	407	1	GFPE_MOUSE
22	284.5	15.4	393	1	BMP2_HUMAN
23	284	15.3	396	1	BMP2_MOUSE
24	283	15.3	394	1	BMP2_RAT
25	281	15.2	374	1	BMP2_BOVIN
26	271.5	14.7	395	1	BMP2_MOUSE
27	270	14.6	375	1	BMP2_BOVIN
28	267	14.4	357	1	GFPI_MOUSE
29	267	14.4	375	1	GFPI_MOUSE
30	264	14.3	375	1	GFPI_MOUSE
31	264	14.3	375	1	GFPI_MOUSE
32	261	14.1	376	1	GFPI_MOUSE
33	261	14.1	376	1	GFPI_MOUSE

34	261	14.1	398	1	BMP2_XENLA
35	259	14.0	375	1	GFPE_PAPIA
36	257	13.9	375	1	GFPE_MOUSE
37	256.5	13.9	376	1	GFPE_RAT
38	256	13.8	375	1	GFPE_CHICK
39	253	13.7	372	1	GFPI_HUMAN
40	247	13.4	345	1	GFPE_RAT
41	246.5	13.3	353	1	BMP2_CHICK
42	246	13.3	398	1	BMP2_XENLA
43	241.5	13.1	355	1	DVPL_BRARE
44	240.5	13.0	399	1	BMP2_MOUSE
45	240	13.0	408	1	BMP2_DANDA

ALIGNMENTS

RESULT 1
ID IHBC_HUMAN STANDARD: PRT: 352 AA.
AC P55103;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 41, Last annotation update)
DE Inhibin beta C chain precursor (Activin beta-C chain).
GN INHBC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI:taxid=9606;
NM (1)
NM SEQUENCE FROM N.A.
RP TISSUE-LIVER;
RC MEDLINE=95126961; PubMed=7826378;
RX Hooten G., Neidhardt H., Schneider C., Pohl J.;
RA "Cloning of a new member of the TGF-beta family: a putative new
RT activin beta C chain.";
RL Biochem. Biophys. Res. Commun. 206:608-613(1995).
RN (2)
RP TISSUE SPECIFICITY.
RX MEDLINE=98089987; PubMed=9428386;
RA Thomas T.Z., Chapman S.M., Hong W., Gursingthe C., Mellor S.L.,
RA Fletcher R., Pedersen J., Ristridger G.P.;
RT "Inhibins, activins, and follistatins: expression of mRNAs and
cellular localization in tissues from men with benign prostatic
hyperplasia.";
RL Prostate 34:34-43(1998).
RN (3)
RP FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -I- SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH
CC ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.
CC ACTIVINS ARE HOMODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT (BY
CC SIMILARITY).
CC -I- TISSUE SPECIFICITY: EXPRESSED IN BENIGN PROSTATIC HYPERPLASIA.
CC -I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC or send an email to license@sib-sib.ch).
CC EMBL: X82540; CAA57890.1; .

DR HSSP: P18075; 1BMP.
 DR MIM: 601233; .
 DR InterPro: IPR002400; GF_cyskn0t.
 DR InterPro: IPR001318; Inhibin_betaC.
 DR InterPro: IPR001839; TGF-beta.
 DR Pfam: PF000019; TGF-beta; 1.
 DR PRINTS: PR00438; GFCYSKN0T.
 DR PRINTS: PR00672; INHIBINBC.
 DR ProDom: PD000357; TGF-beta; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF-BETA_1; 1.
 KM Growth factor: Hormone; Glycoprotein; Signal.
 FT SIGNAL 1
 FT PROPEP 18
 FT CHAIN 19
 FT DISULFID 237
 FT DISULFID 240
 FT DISULFID 247
 FT DISULFID 276
 FT DISULFID 280
 FT DISULFID 316
 FT CARBOHYD 110
 FT CARBOHYD 143
 FT CARBOHYD 161
 SQ SEQUENCE 352 AA; 38238 MW; 496476ADB2562D3E CRC64;

Query Match
 Best Local Similarity 100.08; Score 1849; DB 1; Length 352;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWSLLAFLLAPTTVTPRAGGCGPTLESGRELLDLAKRSLDKLHTOR 60
 DB 1 MWSLLAFLLAPTTVTPRAGGCGPTLESGRELLDLAKRSLDKLHTOR 60
 QY 61 PLNRPVSAALRTALQHLHGVPCALLDNRQECETISFAETGLSTINRLDFESS 120
 DB 61 PLNRPVSAALRTALQHLHGVPCALLDNRQECETISFAETGLSTINRLDFESS 120
 QY 121 DRTAGDREVOASLMFVQLPSNTTWLTKYVYLGLPHNNTLATQYLEVDASGHOL 180
 DB 121 DRTAGDREVOASLMFVQLPSNTTWLTKYVYLGLPHNNTLATQYLEVDASGHOL 180
 QY 121 DRTAGDREVOASLMFVQLPSNTTWLTKYVYLGLPHNNTLATQYLEVDASGHOL 180
 DB 121 DRTAGDREVOASLMFVQLPSNTTWLTKYVYLGLPHNNTLATQYLEVDASGHOL 180
 QY 181 PLGPEPAQAASQGHITLVLGGOVAAOSVLLGSAHRPFAARVRVGRGKHQIRGIDC 240
 DB 181 PLGPEPAQAASQGHITLVLGGOVAAOSVLLGSAHRPFAARVRVGRGKHQIRGIDC 240
 QY 241 OGGSMMCCROEFVDFEIRIGMHDIIPREGYANMFCTGGCPPLHAGMPGIAASFHTAVLN 300
 DB 241 OGGSMMCCROEFVDFEIRIGMHDIIPREGYANMFCTGGCPPLHAGMPGIAASFHTAVLN 300
 QY 301 LKANTAGTTGGGSCCVPTARRPLSLYYDRDSNTYKTDIPMAYVEACGCS 352
 DB 301 LKANTAGTTGGGSCCVPTARRPLSLYYDRDSNTYKTDIPMAYVEACGCS 352

RESULT 2

ID IHBC_MOUSE STANDARD; PRT; 352 AA.
 AC PS5104; 061452;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibin beta C chain precursor (Activin beta-C chain).
 CN INHBC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Liver;
 RX MEDLINE=96435913; PubMed=8838799;
 RA Schmitt J., Hoellen G., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 Pohl J., Schrewe H.;

RT "Structure, chromosomal localization, and expression analysis of the
 RT mouse inhibin/activin beta C (Inhbc) gene.";
 RL Genomics 32:358-366(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96283807; PubMed=8679697;
 RA Lau A.L., Nishimori K., Matzuk M.M.;
 RT "Structural analysis of the mouse activin beta C gene.";
 RL Biochim. Biophys. Acta 1307:145-148(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224404; PubMed=9070865;
 RA Fang J., Wang S.Q., Smiley E., Bonadio J.;
 RT "Genes coding for mouse activin beta C and beta E are closely linked
 RT and exhibit a liver-specific expression pattern in adult tissues.";
 RL Biochem. Biophys. Res. Commun. 231:655-661(1997).
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
 CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
 CC ACTIVINS.
 CC -1- SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH
 CC ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.
 CC ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY
 CC SIMILARITY).
 CC -1- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE ADULT LIVER.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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Query Match 75.3%; Score 1392; DB 1; Length 352;
 Best Local Similarity 75.9%; Pred. No. 1.7e-119;
 Matches 268; Conservative 32; Mismatches 51; Indels 2; Gaps 2;

1 MTSSLLAFLAFLAFTVATPRAGGCGPACGPTLELESORELLDLAKRSILDKLHLTOR 60
 1 MASSLLALLFLTLPTVAVNKGTEGPCPCACGAIPLDESORELLDLAKRSILDKLHLTOR 60
 61 PTLNRPVSRALRALQHLHGVPOGALLE-DNREOBCEIISFAEGSLSTINOTRLDFHSS 119
 61 PTLNRPVSRALRALQHLHGVPOGALLE-DNREOBCEIISFAEGSLSTINOTRLDFHSS 120
 120 SDRTAGDREVOQASLMFVQPLPSNTWTTLKRVNLVGLPHNTLTLATQVLEVDASGMHO 179
 121 G-RMAGSEVQRTQRFMEFVQFPHNATQTMNIRVLRPDTLTLTQVYVANSNGWQ 179
 180 LPLGPEAOAASOGHLLLELVLEGVQVASSVILGGAHRRPFAARVVGKQIHRGID 239
 180 LPLGPEAOAASOGHLLLELVLEGVQVASSVILGGAHRRPFAARVVGKQIHRGID 239
 240 CGGSRMCCROEFVDFREIGMDWITIOPEGYAMNCTGCPHVAAGMGSISFHTAVL 299
 240 CGGSRMCCROEFVDFREIGMDWITIOPEGYAMNCTGCPHVAAGMGSISFHTAVL 299
 300 NLKANTAACTGGSCCVPTARRPLSLYYDRDSNVKTDIPDMVVEACGS 352
 300 NLKANTAACTGGSCCVPTARRPLSLYYDRDSNVKTDIPDMVVEACGS 352

RESULT 3
 ID IHBG_RAT STANDARD: PRT: 351 AA.

16-OCT-2001 (Rel. 40, Created)
 16-OCT-2001 (Rel. 40, Last sequence update)
 16-OCT-2001 (Rel. 40, Last annotation update)
 Inhibin beta C chain precursor (Activin beta-C chain).
 INHBC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCB1;TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar;
 RA Rossmuth W., Peter B., Schulte-Hermann R.;
 RT "Rat activin beta C and beta E: sequence and expression."
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
 RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
 CC EMBRYONIC AXIAL DEVELOPMENT, INSULIN SECRETION, NERVE CELL SURVIVAL,
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
 CC ACTIVINS.
 CC -1- SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH
 CC ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.
 CC ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).

EMBL: AF140031; AAD30132.1; .
 DR HSP: P18075; 1BMP.
 DR InterPro: IPR002405; Inhibin_alpha.
 DR InterPro: IPR001318; Inhibin_betaC.
 DR InterPro: IPR001839; TGF-beta.
 DR Pfam: PF00019; TGF-beta; 1.
 DR PRINTS: PR00669; INHIBINA.
 DR PRINTS: PR00672; INHIBINB.
 DR ProDom: PD000357; TGF-beta; 1.
 DR SMART: SM00204; TGF-beta; 1.
 DR PROSITE: PS00250; TGF-beta; 1.
 DR Growth factor: Hormone; Glycoprotein; Signal.
 KW SIGNAL.
 FT PROPEP 19 236
 FT CHAIN 237 351
 FT DISULFID 239 246
 FT DISULFID 246 316
 FT DISULFID 275 348
 FT DISULFID 279 350
 FT CARBOHYD 110 110
 FT CARBOHYD 142 142
 FT CARBOHYD 160 160
 SQ SEQUENCE 351 AA; 39335 MW; 6B219BF6C3E180A1 CRC64;

Query Match 74.6%; Score 1379.5; DB 1; Length 351;
 Best Local Similarity 75.6%; Pred. No. 2.4e-118;
 Matches 266; Conservative 30; Mismatches 55; Indels 1; Gaps 1;

1 MTSSLLAFLAFLAFTVATPRAGGCGPACGPTLELESORELLDLAKRSILDKLHLTOR 60
 1 MASSLLALLFLTLPTVAVNKGTEGPCPCACGAIPLDESORELLDLAKRSILDKLHLTOR 60
 61 PTLNRPVSRALRALQHLHGVPOGALLE-DNREOBCEIISFAEGSLSTINOTRLDFHSS 120
 61 PTLNRPVSRALRALQHLHGVPOGALLE-DNREOBCEIISFAEGSLSTINOTRLDFHSS 119
 121 DRTAGDREVOQASLMFVQPLPSNTWTTLKRVNLVGLPHNTLTLATQVLEVDASGMHO 180
 121 DRTAGDREVOQASLMFVQPLPSNTWTTLKRVNLVGLPHNTLTLATQVLEVDASGMHO 179
 120 DRTAGDREVOQASLMFVQPLPSNTWTTLKRVNLVGLPHNTLTLATQVLEVDASGMHO 179
 181 PPLGPEAOAASOGHLLLELVLEGVQVASSVILGGAHRRPFAARVVGKQIHRGIDC 240
 181 PPLGPEAOAASOGHLLLELVLEGVQVASSVILGGAHRRPFAARVVGKQIHRGIDC 239
 240 CGGSRMCCROEFVDFREIGMDWITIOPEGYAMNCTGCPHVAAGMGSISFHTAVL 300
 240 CGGSRMCCROEFVDFREIGMDWITIOPEGYAMNCTGCPHVAAGMGSISFHTAVL 299
 300 NLKANTAACTGGSCCVPTARRPLSLYYDRDSNVKTDIPDMVVEACGS 352
 300 NLKANTAACTGGSCCVPTARRPLSLYYDRDSNVKTDIPDMVVEACGS 351

RESULT 4
 ID IHBG_HUMAN STANDARD: PRT: 350 AA.

16-OCT-2001 (Rel. 40, Created)
 16-OCT-2001 (Rel. 40, Last sequence update)
 16-OCT-2001 (Rel. 40, Last annotation update)
 Inhibin beta E chain precursor (Activin beta-E chain).
 INHE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1;TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Rhabdomyosarcoma;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,

DR EMBL, BC005161, AA005161.1; -,
DR InterPro: IPR002405; Inhibin_alpha,
DR InterPro: IPR00318; inhibin_betaC,
DR InterPro: IPR001839; TGF-beta,
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00669; INHIBINA.
DR PRINTS: PR00672; INHIBINBC.
DR Prodom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGFB; 1.
DR PROSITE, PS00250; TGF_BETA_1; 1.
KM Growth factor; Hormone; Glycoprotein; Signal.
FT SIGNAL 1
FT PROPEP 20 236
FT CHAIN 237 350
FT DISULEPID 240 248 INHIBIN BETA E CHAIN.
FT DISULEPID 247 315 BY SIMILARITY.
FT DISULEPID 276 347 BY SIMILARITY.
FT DISULEPID 280 349 BY SIMILARITY.
FT DISULEPID 314 314 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 198 198
SQ SEQUENCE 350 AA: 38561 MW: 449C1495677E3EEF CRC64; N-LINKED (GLCNAC, ...) (POTENTIAL).

14;

RP SEQUENCE FROM N.A.
RA MEDLINE=97224404; PubMed=9070865;
RX Fang J., Wang S.O., Smiley E., Bonadio J.;
RT "genes coding for mouse activin beta C and beta E are closely linked
PT and exhibit a liver-specific expression pattern in adult tissues.";
RL Biochem. Biophys. Res. Commun. 231:655-661(1997)
C -1- FUNCTION: INHIBITS AND ACTIVATES INHIBITAND CONTAINS

RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE

FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION, GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, ERTHOID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPOSE THE FUNCTIONS OF ACTIVINS.

ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY CIVITARELLA)

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MOD; MGI:109289; InM6.
InterPro; IPR002400; GF_cysknot.

PRINTER; PRO0438; GFCYSKNOT.

SMART; SM00204; TGF β ; 1.
PROSITE; PS00250; TGF β _BETA_1;

SIGNAL	1	44	POTENTIAL.
PROPEP	22	236	POTENTIAL.

DISULFID	247	248	BI SIMILARITY.
DISULFID	247	315	BY SIMILARITY.


```

CC CC CONNANL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC CC ACTIVINS.
CC CC
CC CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC CC
CC CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC CC
CC CC ACTIVIN A IS A HOMODIMER OF BETA-A.
CC CC ACTIVIN B IS A HOMODIMER OF BETA-B.
CC CC
CC CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC CC
CC CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC CC
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CC CC
CC CC EMBL; M31669; AAA59451.1; -.
CC CC
CC CC EMBL; M31668; AAA59451.1; JOINED.
CC CC
CC CC EMBL; M31682; AAA59170.1; -.
CC CC
CC CC EMBL; M1437; AAA59169.1; -.
CC CC
CC CC PIR; C24248; C24248.
CC CC
CC CC HSSP; P18075; IBM.
CC CC
CC CC MIM; 147390; -.
CC CC
CC CC InterPro: IPR002400; GF_Cys_knot.
CC CC
CC CC InterPro: IPR000381; Inh1bin_deta.
CC CC
CC CC InterPro: IPR001839; TGF-beta.
CC CC
CC CC InterPro: IPR001111; TGFb_N.
CC CC
CC CC Pfam; PF00019; TGF-beta; 1.
CC CC
CC CC Pfam; PF00688; TGFb_propeptide; 1.
CC CC
CC CC PRINTS; PR00438; GRCYSKNOT.
CC CC
CC CC PRINTS; PR00671; INH1BINB.
CC CC
CC CC ProDom; PD000357; TGF-beta; 1.
CC CC
CC CC SMART; SM00204; TGB; 1.
CC CC
CC CC PROSITE; PS00250; TGF-BETA_1; 1.
CC CC
CC CC Growth factor; Hormone; Glycoprotein; signal.
CC CC
CC CC SIGNAL 1 28 POTENTIAL.
CC CC
CC CC PROPEP 29 292 POTENTIAL.
CC CC
CC CC CHAIN 293 407 INHIBIN BETA B CHAIN.
CC CC
CC CC FT DISULFID 296 304 BY SIMILARITY.
CC CC
CC CC FT DISULFID 303 372 BY SIMILARITY.
CC CC
CC CC FT DISULFID 332 404 BY SIMILARITY.
CC CC
CC CC FT DISULFID 336 406 BY SIMILARITY.
CC CC
CC CC FT DISULFID 371 371 INTERCHAIN (BY SIMILARITY).
CC CC
CC CC CARBOHD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC
CC CC CONFLICT 47 47 S -> A (IN REF. ?).
CC CC
CC CC SEQUENCE 407 AA; 45121 MW; 90316C8357BA6B4 CnC64;
CC CC
CC CC Query Match 32.4%; Score 599.5; DB 1; Length 407;
CC CC Best Local Similarity 36.6%; Pred. No. 3; 9e-47;
CC CC Matches 145; Conservative 60; Mismatches 118; Indels 73; Gaps 16

```

[illegible]

DR InterPro: IPR002400; GF_cysknot.
 DR InterPro: IPR001839; TGF-beta.
 DR InterPro: IPR001131; TGF-beta.
 DR Pfam: PF000019; TGF-beta.1.
 DR Pfam: PF000688; TGF-beta.1.
 DR PRINTS: PR00438; TGF-beta.1.
 DR ProDom: PD000357; TGF-beta.1.
 DR SMART: SM00204; TGF-beta.1.
 DR PROSITE: PS00250; TGF-beta.1.
 DR Growth factor: Hormone; Glycoprotein; Signal.
 DR SIGNAL: 1
 FT PROPEP 26
 FT CHAIN 276
 FT DISULFID 280
 FT DISULFID 287
 FT DISULFID 316
 FT DISULFID 320
 FT DISULFID 355
 FT CARBOHYD 77
 FT CONFLICT 30
 SO SEQUENCE 391 AA; 43608 MW; 060017BF33F7AF6C CRC64;

Query Match 32.3%; Score 598; DB 1; Length 391;
 Best Local Similarity 34.8%; Pred. No. 5.1e-47;
 Matches 136; Conservative 69; Mismatches 138; Indels 48; Gaps 11;

QY 1 MTSSLLAFLLAPTTATPRAGQ---CPACGPTLEESQRE-LILDIAKRIIDK 54
 DB 10 LAALLAGCLLLGAAATPPPPAGSSPDCTSCGFRPEPEKVDGLLEAVKRIILSR 69
 QY 55 LHLTORPLNRPVRAALRFALOHLHVPQALLENR-----EQECE 97
 DB 70 LOMDRRITHAVKAMVTAALKKLAH---GKVEDGKREIPLSDQASAGPAHDPVSE 126
 QY 98 IISFAETGLSTINQRLDFHSSDRTAGRE--VOQASLMFVQ-----LPSNTWTILKY 150
 DB 127 IISFAETDGLASSRVRLYFISNE---GNQNLFFVQASLMVILKILPYLENGSRKRYAV 183
 QY 151 RVLVLGHNTNLTAQVLYLEVASGWHQLPCEPAQASGCHLTLELVLEGVQAQSV 210
 DB 184 KVFYQDPDTSKMNVVEKKVDLRSQMTFPMTEATQALFERGERLINDVQCECEEYS 243
 QY 211 IL-----GGAHRRPFAARVAVG-GKHQIRHRIQCGSGHRCROEFVDFRIGIHD 263
 DB 244 VLPYVDPGESHRLPVYVARADKKHRIKRGLECDGRTVLCRQOQYIDRLIGNND 303
 QY 264 WIQPEYANRPGICGPHIAGPGIATSFHTAVNLKANTAGTTCG--GSCCVPTA 321
 DB 304 WIAPSGYGNVCEGSCPAYLAGVPGSASSFHTAVNQYRMR---GLNPGTVNSCIPITK 360
 QY 322 RRLSLLYDRSDINIKTDIPKVVVAGCS 352
 DB 361 LSTMSMLTFDEDEYNIYKRDVPMNIYECCCA 391

RESULT 10
 ID IHHB_PIG STANDARD; PRT: 349 AA.
 AC P04088;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibin beta B chain precursor (Activin beta-B chain) (Fragment).
 GN IHHB.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 RN NCBL_184823;
 RX NCBI_184823;
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovarian follicular fluid;
 RA MEDLINE-86092207; PubMed-2417121;
 RA Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,

RA Guillemin R., Miall H., Seeburg P.H.;
 RT "Complementary DNA sequences of ovarian follicular fluid inhibin show
 RT precursor structure and homology with transforming growth
 RT factor-beta";
 RL Nature 318:659-663(1985).

RP SEQUENCE OF 235-249.
 RX MEDLINE-92355604; PubMed-1644823;
 RA Nakamura T., Asashima M., Eto Y., Takio K., Uchiyama H., Moriya N.,
 RA Arizumi T., Yashiro T., Sugino K., Titani K., Sugino H.;
 RL "Isolation and characterization of native activin B";
 J. Biol. Chem. 267:16385-16389(1992).

- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
 RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
 INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
 FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
 GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
 EMBRYONIC DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
 SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
 ACTIVINS.

- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
 INHIBIN B IS A DIMER OF ALPHA AND BETA-B.

ACTIVIN A IS A HOMODIMER OF BETA-A.
 ACTIVIN B IS A HOMODIMER OF BETA-B.
 ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
 - SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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 CC or send an email to license@isb-sib.ch).

DR EMBL: X03267; CAA37021.1;
 DR PIR: A01394; WFGGB.
 DR HSSP: P18075; IBMF.

DR InterPro: IPR001839; TGF-beta.
 DR InterPro: IPR001131; TGF-beta.
 DR Pfam: PF000019; TGF-beta.1.
 DR Pfam: PF000688; TGF-beta.1.
 DR ProDom: PD000357; TGF-beta.1.
 DR SMART: SM00204; TGF-beta.1.
 DR PROSITE: PS00250; TGF-beta.1.
 DR Growth factor: Hormone; Glycoprotein.
 FT NON-TER 1

FT PROPEP 234
 FT CHAIN 235
 FT DISULFID 238
 FT DISULFID 245
 FT DISULFID 274
 FT DISULFID 278
 FT DISULFID 313
 FT CARBOHYD 35
 SO SEQUENCE 349 AA; 39354 MW; C571EA91ADA5DE77 CRC64;

Query Match 31.7%; Score 587; DB 1; Length 349;
 Best Local Similarity 37.7%; Pred. No. 4.5e-46;
 Matches 129; Conservative 62; Mismatches 109; Indels 42; Gaps 9;

QY 44 LDIAKRSILDKLHLPORPLNRPVRAALRFALOHLHVPQALLENR-----92
 DB 17 LEAVVRHILNRLQMGGRNITHAVKAMVTAALKKLAH---GKVEDGKREIPLSDQASAGPAHDPVSE 73
 QY 93 -----EQECEIISFAETGLSTINQRLDFHSSDRTAGRE--VOQASLMFVQ-----139
 DB 74 PGADQOERSEIISFAETGLASSRVRLYFISNE---GNQNLFFVQASLMVILKILPYLENGSRKRYAV 130
 QY 140 LPSNTWTILKYRVLVLGHNTNLTAQVLYLEVASGWHQLPCEPAQASGCHLTLELVLEGVQAQSV 199

Db 131 LEKSGRRKRVKVVYQEPBGHGRDMDVNEKRVLDKRSQWHTLPLTEALQALFERGERLNTL 190
 QY 200 VLEGQVASSVIL-----GGAHRRPVAARVRVG-GKHQIHRGICDGGSRMCCROEF 252
 Db 191 DVQDCGCGELAVPVVFDGSESHRPFVYVQARLDSRHRLKRGLEDCGRNLCCROOF 250
 QY 253 FVDFREIGHDMVTOEGVAMNFCIGCCPLHTAGMPCIAASHTVNLMLANTAGCTG 312
 Db 251 FIDFRIGMSDWIAPTGYGNGECSCPAVYACVPGSASSTFTAVVQYRR--GLNP 307
 QY 313 G--GCCVPTARRPLSLLYYDRSDNIVKTDIPDMVEACGCS 352
 Db 308 GTVNSCCIPFKLSTMSMLTFEDDEYNIVKRDVPMIVEECGCA 349

RESULT 11
 ID INHA_PIG STANDARD: PRT: 424 AA.
 AC P03970:
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibin beta A chain precursor (Activin beta-A chain).
 GN INHBA.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Follicular fluid;
 RX MEDLINE=86092207; PubMed=2417121;
 RA Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,
 RA Guillemin R., Nall H., Seeburg P.H.;
 RT *Complementary DNA sequences of ovarian follicular fluid inhibin show
 RT precursor structure and homology with transforming growth
 RT factor-beta*;
 RL Nature 318:659-663(1985).
 RN [2]
 RP SEQUENCE OF 309-323.
 RC TISSUE-Follicular fluid;
 RX MEDLINE=92355604; PubMed=1644823;
 RA Nakamura T., Asashima M., Eto Y., Takio K., Uchiyama H., Moriya N.,
 RA Arizumi T., Yasuiro T., Sugino K., Tlcanl K., Sugino H.;
 RT *Isolation and characterization of native activin B*;
 RL J. Biol. Chem. 267:16385-16389(1992).
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
 CC RESPECTIVELY, THE SECRETION OF FOLITROPIN BY THE PITUITARY GLAND.
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
 CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
 CC ACTIVINS.
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: X03266; CAA27020.1;
 DR PIR: A01393; WPPGBA.

DR HSSP: P18075; 1BMP.
 DR InterPro: IPR002400; GF_cysknct.
 DR InterPro: IPR000491; Inhibin_betaA.
 DR InterPro: IPR001839; TGF-beta.
 DR InterPro: IPR001111; TGF-beta.
 DR Pfam: PF00019; TGF-beta.1.
 DR Pfam: PF00688; TGF-beta_propeptide.1.
 DR PRINTS: PR00438; GFCYSKNCT.
 DR PRINTS: PR00670; INHIBINBA.
 DR ProDom: PD000357; TGF-beta.1.
 DR SMART: SM00204; TGF-beta.1.
 DR PROSITE: PS00250; TGF-Beta_1.
 DR Growth factor: Hormone; Glycoprotein; Signal.
 KW SIGNAL
 FT SIGNAL 1 20
 FT PROPEP 21 308
 FT CHAIN 309 424
 FT DISULFID 312 320
 FT DISULFID 319 389
 FT DISULFID 348 421
 FT DISULFID 352 423
 FT DISULFID 388 388
 FT CARBOHYD 165 165
 SQ SEQUENCE 424 AA; 47476 MW; 436BC6226FDAF52 CRC64;

Query Match 30.4%; Score 562; DB 1; Length 424;
 Best Local Similarity 31.2%; Pred. No. 1, 1e-43;
 Matches 131; Conservative 69; Mismatches 142; Indels 78; Gaps 10;

QY 6 LLATLLAPTTVATPRAG-----GCPACGGPTL--ELDSORELLDLKRSILDKLTLT 58
 Db 10 LLASCSWITVNSPTPGSGGSAAPDCPSALATLPRDVPROPEPEAVKAKHILMLHLK 69
 QY 59 QPPLNRPVSRALRLALQHL-----GVPDGLLEDNRQECETISPAET 104
 Db 70 KRPTQVQVPAALALNLRKHVGKGVENGVELEDDIGRAEMNLMTSEIITFAEA 129
 QY 105 GLSTINOTRLDFHSSRTACDRE-VQQAALMFVQVLPSTTTTLKVRVLYLG----- 156
 Db 130 GTA-----RKTLEIREISKEGSDLSVERAEIWLFLKPKANRTRTVIRLQPOORRPG 184
 QY 157 -----PHNTMLTATQYLLEVDASGWHQPLTPEAQ-----AAC 190
 Db 165 SADAGEAEADYGFPEKSEVILSEKVVDAKRTWHIFPVSSIQRLDQCKSALDRTAC 244
 QY 191 SOGHLT-LELVLEGQVASSVILG-----AAHRRPVAARVRVGK--HQ 232
 Db 245 EQCHETGASLVLLGKKKKKEEADGKRDEGAGVDEKESHRPFLMLQAROSEHPHR 304
 QY 233 IHRGIDCGSRMCCROEFVDFREIGHDMVTOEGVAMNFCIGCCPLHAGMPCIAA 292
 Db 305 RRRGLECDGKVNCCCKKQFVSRDGMNDMLTAPSGYANVCGECPHIACTGSSSL 364
 QY 293 SFHTAVNLMLKANTAGTGGSCVPTARRPLSLLYYDRSDNIVKTDIPDMVEACGCS 352
 Db 365 SFHSVIVNHMYRMRGHSPPANLKSQCVPTKLPRMSMLVYDDQONIKKDIONMIVEECGS 424

RESULT 12
 ID INHA_RAT STANDARD: PRT: 424 AA.
 AC P18331:
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibin beta A chain precursor (Activin beta-A chain).
 GN INHBA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91042598; PubMed=3153478;

Db	184	GSIDMCDEAEEMGLKJERSELLSKYVDARKSMHIFPPVSSSTRQRLDQKSSLDVRIA	243
Qy	203	GVYAGSS-----VILG-----	GAARFP--VAARVGVGKH 231
Db	244	CEQCQSGASLVLLKKKKKEVDGDKKKDSDGLSEEEKSHRPFMLLAQNSGDHPH	303
Qy	232	QIARRGIDACGSGSMCCROEFFVDFREITGMWDVITQPEGYAMNFCJGGCPYLHAGMPGA	291
Db	304	RRRRRGLECDGVKNVCKKQKFFVSRKDGIMWDVILASGHNAYCSECSPIHAGSGSS	363
Qy	292	ASHTFVLLKLANPAAGTTGGGSCVPTARPLISLLYDRDSNIYKTDIPMVAEAGCC	351
Db	364	LSRHSFTVNHMYRMGRHSPFANLKSCCVPTKLRPWSMLYDGDGNITKIDQNIWIVEGCG	423
Qy	352	S 352	
Db	424	S 424	
RESULT 13			
INBA_HORSE			
ID	INBA_HORSE	STANDARD:	PRT: 426 AA.
AC	P55102:		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Inhibin beta A chain precursor (Activin beta-A chain).		
GN	INBA.		
OS	Equus caballus (Horse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.		
OX	NCBI_Taxid=9796;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Ovary;		
RX	MEDLINE=96031670: Pubmed-7548399;		
RA	Yoshida S., Yamamouchi K., Hasegawa T., Ikeda A., Suzuki M.,		
RT	Chang K., Matsuyama S., Nishihara M., Takahashi M.;		
RT	"Molecular cloning of cDNA for equine ovarian inhibin/activin beta A		
RT	subunit."		
RL	J. Vet. Med. Sci. 57:469-473(1995).		
CC	-I- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,		
CC	RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.		
CC	INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE		
CC	FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,		
CC	GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,		
CC	ERTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,		
CC	EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR		
CC	SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF		
CC	ACTIVINS.		
CC	-I- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.		
CC	INHIBIN A IS A DIMER OF ALPHA AND BETA-A.		
CC	INHIBIN B IS A DIMER OF ALPHA AND BETA-B.		
CC	ACTIVIN A IS A HOMODIMER OF BETA-A.		
CC	ACTIVIN B IS A HOMODIMER OF BETA-B.		
CC	ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.		
CC	-I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.		
CC	-----		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; D50326; BAA08652.1; -.		
DR	HSSP; P18075; 1BMP.		
DR	InterPro; IPR002400; GF_cysknot.		
DR	InterPro; IPR000491; Inhibin_Delta.		
DR	InterPro; IPR001839; TGF-beta.		
DR	InterPro; IPR001111; TGFb_N.		
DR	Pfam; PF000019; TGF-beta; 1.		

DR pfam: PF00688; TGF-beta; propeptide; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR PRINTS: PR00670; INHIBINB.
 DR PRODOM: PD000357; TGF-beta; 1.
 DR SMART: SM00204; TGF-beta; 1.
 DR PROSITE: PS00250; TGF-beta; 1.
 DR Growth factor; Hormone; Glycoprotein; Signal.
 FT SIGNAL 1 20
 FT PROPEP 21 310
 FT CHAIN 311 426
 FT DISULFID 314 322
 FT DISULFID 321 391
 FT DISULFID 350 423
 FT DISULFID 354 425
 FT DISULFID 390 390
 FT CARBOHYD 165 165
 FT SEQUENCE 426 AA; 47709 MW; E481060B8368A77D CRC64;
 Query Match 30.38; Score 560; DB 1; Length 426;
 Best Local Similarity 32.58; Pred. No. 1.7e-43;
 Matches 137; Conservative 67; Mismatches 138; Indels 80; Gaps 12;
 QY 6 LLAFLAFLAFTVATPRAG-----QCPACGPTL--ELESORELLDLAKRSILDKLHLT 58
 DB 10 LLAFLAFLAFTVATPRAG-----QCPACGPTL--ELESORELLDLAKRSILDKLHLT 58
 QY 59 QPRLNRPVSRALRTALQHLH-----GVPOGALLEDRQECETISFAET 104
 DB 70 KRPDVTQPVKPAALNLRKLVKGVKGVENGVEIEDDGRRAEMELMDOTSETITFAES 129
 QY 105 GLSTINTRLDFHSSRTAGDRE--VOQASLMFVQLPSTWTWTLKRVVLV-----G 156
 DB 130 GTA-----RRTLHEISKESGSLVERAEVWLFVLPKANRRTKRVTRIRLQOQKHPOG 184
 QY 157 PHTNLTLATQYLE-----VDA--SGMHLPLGPEAQAACSGCHLTLELVLE- 202
 DB 185 SSDREAEAEADLMERSSEQLISKVVDARKSTMHIFPVSSSIQRLDQKSSLDIRIAC 244
 QY 203 ---GVQAOSSVYLQ-----GA-----AHNRP--VAARVAVGSK 230
 DB 245 DQCHETGASLVLLGKKKKKEEGCKKKKDGEGAGVDEKEOSHNPFLMLQKROSEDHP 304
 QY 231 HOHRRIGIDCGGSRMCCROEFYDFREIGMHMMIIOPEGYANPFIQGCPLTIAGMPGI 290
 DB 305 HRRRRRIGIECGKVNICKKQKFYSFKIDGNDMIIIPSYIHANVCEGECPSHIACTSGS 364
 QY 291 AASFHTAVLNLKANTAGATTGGSCCVPTARRPLSLIYDRDSNIVKTDIPRVYVAGG 350
 DB 365 SLSFSTVINGYRLRGHNPFANLKSVCPTKLRPMSMLVYDDGONIIKIDQNMVIECG 424
 QY 351 CS 352
 DB 425 CS 426
 RESULT 14
 THBA_MOUSE STANDARD: PRT: 424 AA.
 ID THBA_MOUSE
 AC Q04998;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibin beta A chain precursor (Activin beta-A chain).
 GN INHBA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93321614; Pubmed=8330535;
 RA Albano P.M., Groome N., Smith J.C.;
 RT Activins are expressed in preimplantation mouse embryos and in ES

RT and EC cells and are regulated on their differentiation."
 RL Development 117-711-723(1993).
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
 CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
 CC ACTIVINS.
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
 CC -1- TISSUE SPECIFICITY: UTERUS, OVARY, AND LIVER.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 CC
 DR EMBL: X69619; CAA49325.1; -
 DR PIR: S31440; S31440.
 DR HSSP: P18075; IBM.
 DR MGD: MGI.96570; Inba.
 DR InterPro: IPR002400; GF_cysknol.
 DR InterPro: IPR000491; Inhibin_betaa.
 DR InterPro: IPR001839; TGF-beta.
 DR InterPro: IPR001111; TGF-beta.
 DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGF-beta; propeptide; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR PRINTS: PR00670; INHIBINB.
 DR PRODOM: PD000357; TGF-beta; 1.
 DR SMART: SM00204; TGF-beta; 1.
 DR PROSITE: PS00250; TGF-beta; 1.
 DR Growth factor; Hormone; Glycoprotein; Signal.
 FT SIGNAL 1 20
 FT PROPEP 21 308
 FT CHAIN 309 424
 FT DISULFID 312 320
 FT DISULFID 319 389
 FT DISULFID 348 421
 FT DISULFID 352 423
 FT DISULFID 388 388
 FT CARBOHYD 165 165
 FT SEQUENCE 424 AA; 47392 MW; 80C251B8754A7213 CRC64;
 Query Match 30.28; Score 559; DB 1; Length 424;
 Best Local Similarity 32.18; Pred. No. 2.1e-43;
 Matches 135; Conservative 71; Mismatches 135; Indels 80; Gaps 12;
 QY 6 LLAFLAFLAFTVATPRAG-----QCPACGPTLELE--SORELLDLAKRSILDKLHL 57
 DB 10 LLAFLAFLAFTVATPRAG-----QCPACGPTLELE--SORELLDLAKRSILDKLHL 57
 QY 58 TQPTLNPVSRALRTALQHLH-----GVPOGALLEDRQECETISFAE 103
 DB 69 KRPDVTQPVKPAALNLRKLVKGVKGVENGVEIEDDGRRAEMELMDOTSETITFAE 128
 QY 104 TGLSTINTRLDFHSSRTAGDRE--VOQASLMFVQLP--SNTWT--LKVYVLVGFH-- 158
 DB 129 SGTA-----RRTLHEISKESGSLVERAEVWLFVLPKANRRTKRVTRIRLQOQKHPOG 183
 QY 159 -----NTNLTLATQYLEVDASGNHQLPLGPEAQAACSGCHLTLELVLE 202

DB 184 GSLDTGDEAEENGLKSESELLSEKVVYDARKSTWHIFPVSSSTORLDDOKSSLDVRIA 243
 OY 203 GVOAASS---VILG-----GAHRPP--VAARVRVCGKH 231
 DB 244 CQCCBESGSLVLLGKKKKKEVDGKKKSDSGLEEEKOSHRRPPLMLAORSEDHPH 303
 OY 232 QIHRRGIDCGGSRMCCKQEFFVDREIGWHDWIIIOPEGYAMNCCICDCLHLAGMGIA 291
 DB 304 RRRRRGLRCDGKVNICKCKOFFVSPKIDGMWDIITAPSGHANYCECECPSHIAGTSGSS 363
 OY 222 ASFHNAVNLKANTACTGGSCCPVTPARRPLSLLYDRDSNYKVTIDIPDWVVEACGC 351
 DB 364 LSFHSVTHNYRMGHSPFANLKCSCVPYTKLRFPMMLYDGDGNIITKIDQNNIIVECCG 423
 OY 352 S 352
 DB 424 S 424

RESULT 15
 ID IDBA_HUMAN STANDARD; PRT: 426 AA.
 AC P08476: O14599;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Inhibin beta A chain precursor (Activin beta-A chain) (Erythroid
 DE differentiation protein) (EDF).
 GN INHBA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE-86186863; PubMed-3754442;
 RA Mason A.J., Niall H.D., Seeburg P.H.;
 RT "Structure of two human ovarian inhibins";
 RL Biochem. Biophys. Res. Commun. 135:957-964(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88190086; PubMed-3267209;
 RA Murata M., Eto Y., Shibai H., Sakai M., Muramatsu M.;
 RT "Erythroid differentiation factor is encoded by the same mRNA as that
 RT of the inhibin beta A chain";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:2434-2438(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92135888; PubMed-1777673;
 RA Tanimoto K., Handa S.I., Ueno N., Murakami K., Fukunizu A.;
 RT "Structure and sequence analysis of the human activin beta A subunit
 RT gene";
 RL DNA Seq. 2:103-110(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX Glossip D., Dubuque T., Graves T., Duckles G.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 311-426 FROM N.A.
 RX MEDLINE-87005283; PubMed-3758355;
 RA Stewart A.G., Milbore H.M., Ring J.M., Crowther C.E., Forage R.G.;
 RT Human inhibin genes. Genomic characterisation and sequencing";
 RL FEBS Lett. 206:329-334(1986).
 RN [6]
 RP SEQUENCE OF 311-426 FROM N.A.
 RC TISSUE-Testis;
 RA Berg H., Walter M., Northmann W.;
 RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,

CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
 CC ACTIVINS.
 CC -I- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
 CC -I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).

CC EMBL: M13436; AAA59168.1; -
 CC EMBL: X04447; CAA28041.1; -
 CC EMBL: X57578; CAA40805.1; -
 CC EMBL: X57579; CAA40805.1; JOINED.
 CC EMBL: X57579; CAA40805.1; -
 CC EMBL: AC005027; AAD43185.1; -
 CC EMBL: J03634; AAA35787.1; -
 CC EMBL: A14422; CAA01159.1; -
 CC EMBL: X72498; CAA51163.1; -
 CC PIR: A30884; A30884.
 CC PIR: B24248; B24248.
 CC PIR: B23556; B23556.
 CC PIR: S30488; S30488.
 CC HSSP: P18075; IIBM.
 CC MIM: 147290; -
 CC InterPro: IPR002400; GF_cysknot.
 CC InterPro: IPR000491; Inhibin_beta.
 CC InterPro: IPR001839; TGF-beta.
 CC InterPro: IPR001111; TGFb_N.
 CC Pfam: PRO0019; TGF-beta; 1.
 CC Pfam: PRO0688; TGFb_propeptide; 1.
 CC PRINTS: PRO0438; GFCYSKNOT.
 CC PRINTS: PRO0670; INHIBINBA.
 CC ProDom: PD000357; TGF-beta; 1.
 CC SMART: SM00204; TGFb; 1.
 CC PROSITE: PS00250; TGF_beta_1; 1.
 CC Growth factor; Hormone; glycoprotein; signal.
 CC SIGNAL.
 CC FT SIGNAL 1 20
 CC FT PROPEP 21 310
 CC FT CHAIN 311 426
 CC FT DISULFID 314 322 BY SIMILARITY.
 CC FT DISULFID 321 391 BY SIMILARITY.
 CC FT DISULFID 350 423 BY SIMILARITY.
 CC FT DISULFID 354 425 BY SIMILARITY.
 CC FT DISULFID 390 390 INTERCHAIN (BY SIMILARITY).
 CC FT CARBOHYD 165 165 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CONFLICT 377 379 RMR -> AC (IN REF. 6).
 CC FT SEQUENCE 426 AA; 47442 MW; 201CDEB99CB6919 CRC64;

Query Match 30.18; Score 557; DB 13; Length 426;
 Best Local Similarity 31.58; Pred. No. 3; Le-43;
 Matches 133; Conservative 74; Mismatches 135; Indels 80; Gaps 12;

OY 6 LLAFLLAFTVAVAPRAG-----QCPACGGPTL--ELFSORELLDLAKRSILDKLHLT 58
 DB 10 LLAACWIIIVRSPTPGSGSHAAPDCSCALALPKDVNSQPEWEAVYKHLINMLHLK 69
 OY 59 ORPTLNRPVSAALRTALQLHL-----GVPGALLENRRROCEETISFAET 104
 DB 70 KRPTVQGVPAALALNIRKLHVCKVGENGYVEIEDIGRAENMLMDQTSIIITFAES 129
 OY 105 GLSTINQRLDFHSSRTAGDRE--VQASLAFPEVQLP-SNTTWT-LKRVYLVLPGRH--- 158

Db 130 GTA-----KTLHFEISKEGSDLSVERAEVWLFKVKANRTKVTIRLFQOQKHPOG 184
OY 159 -----NTNLTATQYLLLEVDA SGWHQPLGPEAOACSGHLLLEVL 203
Db 185 SLDTGEAEVEVLKGERSELILSEKVDARKSTWHVPVSSIOILLDOGKSSLDVRIAC 244
OY 204 QVAQSS-----VILG-----GA-----AHRPF--VAARVRVGK 230
Db 245 EDOQESGASLVLLGKKKKKEEGEGKKGGGAGADEKEEQSHRPPLMLQARQSEDPH 304
OY 231 HOIHRGIDCGSGRMCCROEFVDREIGWHDIIOPEGYAMNECIGQCPHIAIMPFI 290
Db 305 HRRRRGLECDGKVNICCKKOFYSEKDIQNDWIIAPSGYHANYCEGECPSHLAGTSGS 364
OY 291 AASFHTAVLNLKANTAGTTGGGSCVPTARRPLSLLYDRDSNIVKTDIPDWVEACG 350
Db 365 SLSEHSTVINHYMRGHSPPANLKSCCVPTKLPRMSMLYYDDGONIIRKIDIONMIVEECG 424
OY 351 CS 352
Db 425 CS 426

Search completed: October 12, 2002, 02:06:54
Job time : 15.5 secs

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OM protein - protein search, using sw model

Run on: October 11, 2002, 23:57:49 : Search time 42 Seconds
(without alignments)
1449.862 Million cell updates/sec

Title: US-09-684-383-2
1849

Perfect score: 1 MTSLLLAFLAFLAFTVATP.....DSNIVKTDIPDMVEACGS 352
Sequence:

Scoring table: BIOSUM62
Gap 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_todent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvires:*
16: sp_bacteriophage:*
17: sp_archaeophages:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	688.5	37.2	367	13 091696	091696 xenopus lae
2	649	35.1	350	11 091KH3	091KH3 mus musculus
3	607.5	32.9	370	13 091350	091350 xenopus lae
4	584.5	31.6	395	13 09PW66	09PW66 anguilla ja
5	573.5	31.0	393	13 090261	090261 brachydanio
6	564	30.5	392	13 09PW88	09PW88 carassius a
7	554	29.0	426	4 09HBP0	09HBP0 homo sapien
8	547	29.6	413	13 098860	098860 cynops pyr
9	533	28.8	424	13 098859	098859 melagris g
10	518	28.0	404	13 09PW65	09PW65 carassius a
11	354	19.1	115	13 09DGE9	09DGE9 cyprinus ca
12	354	19.1	119	6 095KPI	095KPI allurus ful
13	353.5	19.1	119	13 042125	042125 pagrus majo
14	353	19.1	115	13 09DGP1	09DGP1 cyprinus ca
15	353	19.1	115	13 09DGE6	09DGE6 oryzias lat
16	353	19.1	119	6 095N79	095N79 alluropoda

17	353	19.1	119	6 095KPI2	095KPI2 ursus malay
18	352	19.0	138	13 09WGT9	09WGT9 brachydanio
19	347	18.8	115	13 09DGF0	09DGF0 cyprinus ca
20	333	18.0	115	13 09DGE7	09DGE7 oryzias lat
21	329	17.8	115	13 09DGE2	09DGE2 cyprinus ca
22	326	17.6	115	13 09DGE8	09DGE8 oryzias lat
23	323.5	17.5	133	13 09DGT4	09DGT4 oreochromis
24	323	17.5	133	13 0902D1	0902D1 oncorhynch
25	323	17.5	133	13 090W17	090W17 salmo salar
26	320	17.3	133	13 09DGT8	09DGT8 salmo salar
27	319.5	17.3	133	13 09DGT9	09DGT9 morone saxa
28	319.5	17.3	133	13 09DGT8	09DGT8 morone amer
29	317.5	17.2	104	13 098861	098861 cynops pyr
30	317	17.1	377	13 098TB3	098TB3 morone chry
31	312	16.9	373	13 0902D2	0902D2 oncorhynch
32	311	16.8	373	13 098TB3	098TB3 salvelinus
33	309.5	16.7	376	13 09DGT6	09DGT6 umbra cl
34	307	16.6	120	13 09DGT8	09DGT8 brachydanio
35	306.5	16.6	102	13 090388	090388 carassius a
36	305	16.5	389	13 090Y00	090Y00 ictalurus p
37	304.5	16.5	102	13 090389	090389 carassius a
38	296.5	16.0	385	13 090W05	090W05 sparus aur
39	292.5	15.8	102	13 09DGT3	09DGT3 oncorhynch
40	281	15.2	586	5 09VOC9	09VOC9 drosophila
41	280	15.1	102	13 090390	090390 carassius a
42	277	15.0	373	5 061643	061643 drosophila
43	272	14.7	102	13 09DGT1	09DGT1 oncorhynch
44	270	14.6	375	6 095N97	095N97 bos taurus
45	267	14.4	432	13 09PFT9	09PFT9 brachydanio

ALIGNMENTS

RESULT 1

ID 091696 PRELIMINARY: PRT: 367 AA.

AC 091696;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE ACTIVIN D PRECURSOR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=95275314; PubMed=7755637;
RA Oda S., Nishimatsu S., Murekami K., Ueno N.;
RT subunit: a dorsal mesoderm-inducing activity in Xenopus.;
RL Biochem. Biophys. Res. Commun. 210:581-588(1995).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: D49543; BAA08494.1; .
DR HSSP: P12643; BNP.
DR InterPro: IPR002400; GF_CysKnot.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGF-beta.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRODOM: P0000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-beta; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 253 POTENTIAL.
FT CHAIN 254 367 'ACTIVIN D'.
SQ SEQUENCE 367 AA; 41729 MW; CTE6334BD06FA04 CRC64;
Query Match 37.2%; Score 688.5; DB 13; Length 367;

Best Local Similarity 40.4%; Pred. No. 4.5e-58;
Matches 147; Conservative 65; Mismatches 125; Indels 27; Gaps 8;

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OY 5 LLAFLLLAPTTATPRAGGCGPCTLEESQRELLDLAKRSILDKLHTORTPTLN 64
DB 15 LTLGLALAASTOGLTKKS--QCPSCG-----VODKEVMTLEAKQOILQKHLKERENIT 66
OY 65 RPVSRAALRTALQHLH-GVPQAGAL-----EDNRQECETISPAETGLSTING 111
DB 67 HPVPRGAVANALRLHLNKRMEGLFGSNSMDSNTENTDIDQOSYEIISAEIETIENS 126
OY 112 TRLDHFSSORTACDRVQOASLMFFVQLPSNTTWLKVAVLGLPHNTNLATQYILE 171
DB 127 ITLNFQPTDRKEQ-SAHVLOAHMLFEPKANRTSQONETIRLYVQEAYSRRILISEKLE 185
OY 172 VDAAGWHQLPLGPEAOAASOGHLELVEGOVAOSVILGCA--AHRFVAARAVGCG 229
DB 186 PRMTGMOFTSLKSLMLQTFPFGKSKSLQLELNCOCQDVPVLANPNNSHQPVAQAQVHE 245
OY 230 K-HQIHRGIDCOGGRMCCROEFVDFREIGMHWITIOPEGYAMNFCIOCPPLHAGMP 288
DB 246 OSHHATKRSINCQNSMLCCRKDYVDFKIDGNMDIKKEGYQIYCMKGLCPMHITAGAP 305
OY 289 GIASFTAVLNILKANTAGTTGGSCVPTARRPLSLIYDRDSNIYKTDIPDMVVEA 348
DB 306 GMAASFHTVNLNIKANNI--QTAVNSCCVPTKRRLPLSLMLYEDRNNNVLTADIMIVEA 363
OY 349 CGCS 352
DB 364 CGCS 367

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RESULT 2
OY1X3 PRELIMINARY: PRT: 350 AA.
ID OY1X3:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE INHIBIN BETA E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NCBI_TaxID=10090; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN 11
RP SEQUENCE FROM N.A.
RA TISSUE=LIVER;
RA Strusberg R.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
SO EMBL: BC010404; AAH10404.1;
SQ SEQUENCE 350 AA: 39002 MW: 987EABAFAC389FA CRC64;

Query Match 35.1%; Score 649; DB 11; Length 350;
Best Local Similarity 42.4%; Pred. No. 2.7e-54;
Matches 153; Conservative 58; Mismatches 118; Indels 32; Gaps 14;

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OY 6 LLAFLLLAPTTATPRAGGCGPCTLEESQRELLDLAKRSILDKLHTORTPTLN 65
DB 8 LMLDILMALVWQSTRSA--CPSCGPTLAPQGERALVLELAKQOILBESLHLSRPRI 65
OY 66 PVSRAALRTALQHLHGVQALLENRECEIISFA--ETGLSTINOTRLDHFSSDR 122
DB 66 PLQOALVLRALRLO--PK-SWVPGNR--KVISFATIIDKSTSTY-RSMLEFOLS-- 115
OY 123 TAGDREVOOASLMFFVQLPSNTTWLKVAVLGLPHNTNLATQYILE--VDAAGWHQL 180
DB 116 PLMSHNLVHARL--MLHVPSPFTGLYLRIFRCG--TRCRGRFRFLDEHOTTSGMHAL 171
OY 181 PLGPEAOAASOGHLELVEGOVAOSS-----VILGCA--HRRFVAARAVG--GKH 231
DB 172 TLPSGSLRSEDESGVVKLOLEFRPLDLNSTAAGLPRLLDLDGQOQRPFLIKRANPEAG 231
OY 232 QIHRGIDCOGGRMCCROEFVDFREIGMHWITIOPEGYAMNFCIOCPPLHAGMPGIA 291

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DB 232 RARRRPTCEPERPLCCRDHYDPOELGWRDMLDPOBSYQUNYSCGCPPLASPGIA 291
OY 292 ASFTAVLNILKANTAGTTGGSCCVPTARRPLSLIYDRDSNIYKTDIPDMVVEACGC 351
DB 292 ASFSASVFSILKANNP--WPAGSSCCVPTARRPLSLIYDHNNGNVYKTDVPMVVEACGC 349
OY 352 S 352
DB 350 S 350

```

RESULT 3
OY1350 PRELIMINARY: PRT: 370 AA.
ID OY1350:
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ACTIVIN BETA B SUBUNIT.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NCBI_TaxID=8355; Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
OX xenopodinae; xenopus.
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE-93773083; PubMed-8500654;
RA Dohmann C.E., Hemmati-Briyvanlou A., Thomsen G.H., Fields A.,
RA Wolff T.M., Melton D.A.;
RT *Expression of activin mRNA during early development in Xenopus
RT laevis.*
CC Dev. Biol. 157:474-483(1993).
CC 1. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: S61773; AA826863.1;
DR HSSP: P18075; BMP.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGFb_M.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRODOM: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF-BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 370 AA: 41679 MW: AD21502AC45F1DE9 CRC64;

Query Match 32.9%; Score 607.5; DB 13; Length 370;
Best Local Similarity 36.6%; Pred. No. 3e-50;
Matches 140; Conservative 70; Mismatches 122; Indels 51; Gaps 14;

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OY 5 LLAFLLLAPTTATPRAGGCGPCTLEESQRELLDLAKRSILDKLHTORTPTLN 62
DB 4 LLLPLLAGLARTCAPSPPTPEPCPSC-HPPMEPB-----MLEAVKRHLITLLHMQRPN 57
OY 63 LNRPSRAALRTALQHLHGVQALLENRECEIISFA--ETGLSTINOTRLDHFSSDR 104
DB 58 ITHVPRANVSALEKLLHA---GNVREDGNLEIPDLGHSILPPRGHSTENSALITTEAET 114
OY 105 GLSTINOTRLDHFSSDRTAGDRE--VOOASLMFFVQLP--SWTWTWLVAVLGLPHN 159
DB 115 DDVVASRVRSLFTIANE---GNQNLVFGQSLMLYLKLPVEMKSRKRIKRVHFOAFN 171
OY 160 TNLATQYILEVDASGWHQLPLGPEAOAASOG--HLTLELVEGOVAOSSVI-----L 212
DB 172 PDKNMWEKKVDIRSGWHFPLTEALISLEFEEGERLNLEVOCDG--CGEYSVLPVYVD 230
OY 213 GGAHRRPVAVARVVG--GKHQIHRGIDCOGGRMCCROEFVDFREIGMHWITIOPEGY 271
DB 231 GEESHRRPLVYVHARLADNKRIRGRLECDGHNMLCCROQFYIDFRILGNMDWITAPAGY 290
OY 272 AMNFCIOCPPLHAGMPGIAASFTAVLNILKANTAGTTGG--GSCCVPTARRPLSLI 329

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DB 291 YCNVCGSPALACVPGSASFHTAVVNOYRMR---GLNCTVNSCCIPFKLSTMLY 347
 OY 330 YDRSNVKTIDIPDMVVEACGS 352
 DB 348 FDDEYNIVKRDVPMNIVECGCA 370

RESULT 4

O9PMG6 PRELIMINARY: PRT: 395 AA.
 AC O9PMG6: 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ACTIVIN B.
 OS Anguilla japonica (Japanese eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
 OC Anguillidae; Anguilla.
 NCBI_TaxId=7937;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Mura T., Mura C., Eto Y., Nagahama Y.;
 RT "Activin B gene is required for the initiation of spermatogenesis in
 the Japanese eel, Anguilla japonica.";
 RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL: AB025356; BAA83804.1;
 DR HSSP: P12643; 3BMP.
 DR InterPro: IPR000381; Inhibin_beta.
 DR InterPro: IPR001318; Inhibin_beta.
 DR InterPro: IPR001839; TGF-beta.
 DR Pfam: PF000019; TGF-beta_N.
 DR Pfam: PF00688; TGF-beta; 1.
 DR PRINTS: PR00671; INHIBINB.
 DR PRINTS: PR00672; INHIBINB.
 DR ProDom: PD000357; TGF-beta; 1.
 DR SMART: SM00204; TGF-beta; 1.
 DR PROSITE: PS00250; TGF-BETA; 1.
 DR GlycoProtein.
 SO SEQUENCE 395 AA: 43889 MW; FA56D062D18509A3 CRC64;

Query Match 31.6%; Score 584.5; DB 13; Length 395;
 Best Local Similarity 35.2%; Pred. No. 5,4e-48;
 Matches 134; Conservative 67; Mismatches 131; Indels 49; Gaps 12;

OY 13 APPTVATPRAGGCPACGGPTLEESOREL-LIDLAKRSILDKLHTQPTLNRPVSRRA 71
 DB 23 APGETVTSODTCASGGLGPESGRMDIDLEAVKRHLNRLQKREPRNTHPIPKRA 82
 OY 72 LRTALQHLGVPQALLDNR-----EDECIIISFAETGLSTINOTRL 114
 DB 83 MVTALRLKHA---GKVRDEGRVELPMLDGHATYNNVEQEDTSEIISFAES--DELTSKSS 137
 OY 115 DFNH-SSDRTAGREVOQASL-MFVQLP-----SNTITLTKVRLVGLPNNHTNLTLA- 165
 DB 138 SFHFLINNEGONLYVQASLMLFRLPSSAKSGSRKRVTVVYVQGTGAATAAAAAAG 197
 OY 166 -----TOYLLVEDASGWHQPLGPEAQAACSGHLLTLELVLEGQVASSVIL-----CG 214
 DB 198 GRMLVEKREVELKRSQWHTFRLTEPVAGVFERDRQDDVRCGEAANAVALPVLDPGD 257
 OY 215 AARPEVAARVRC-GKHQIHRGIDCGGSRMCCROEFFVDREIGWHDIIOPGCIAM 273
 DB 258 ESHRPFLVQAARLADGKHRIKRLGLEDCTGGLCCROQFYIDRLIGWDMIIAPSGYFG 317
 OY 274 NPGICGCPHLAGMGIAASFHTAVLNLKANTAACTGG--GSCCVPARARPLSLTYD 331
 DB 318 NYCGSCPATVACVPSASSFHTAVVNOYRMR---GMSFQSMNSCIPTRLSLMSMLTYD 374

OY 332 RDSNVKTIDIPDMVVEACGS 352
 DB 375 DEYNIVKRDVPMNIVECGCA 395

RESULT 5

O90261 PRELIMINARY: PRT: 393 AA.
 AC O90261: 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ACTIVIN BETA B.
 GN INHIB OR ZACTBETAB.
 OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Danio.
 NCBI_TaxId=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95011555; PubMed=7926744;
 RA Wildrod J., Frederic R.M.;
 RT "Disruption at mesoderm and axis formation in fish by ectopic
 expression of activin variants: the role of maternal activin.";
 RL Genes Dev. 8:1448-1462(1994).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL: X76051; CAA53636.1;
 DR HSSP: P12643; 3BMP.
 DR ZFIN: ZDB-GENE-990415-2; Inhib.
 DR InterPro: IPR002400; GF_cysknob.
 DR InterPro: IPR001839; TGF-beta.
 DR InterPro: IPR001111; TGF-beta_N.
 DR Pfam: PF000019; TGF-beta; 1.
 DR Pfam: PF00688; TGF-beta; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR ProDom: PD000357; TGF-beta; 1.
 DR SMART: SM00204; TGF-beta; 1.
 DR PROSITE: PS00250; TGF-BETA; 1.
 DR GlycoProtein.
 SO SEQUENCE 393 AA: 43830 MW; FA769C4DBEAD252 CRC64;

Query Match 31.0%; Score 573.5; DB 13; Length 393;
 Best Local Similarity 34.3%; Pred. No. 6,2e-47;
 Matches 134; Conservative 80; Mismatches 128; Indels 49; Gaps 14;

OY 1 MTSLLIAFLILAPTYATPRAG---GCPACGGPTLEESOREL-LIDLAKRSILDKLH 56
 DB 13 LSVTCLMAALLSVQCSLGAETGSOESQVSCGLGHQEDSGRMDIDLEAVKRHLNRLQ 72
 OY 57 LTOPRTLNRPVSRRAALRTALQHLGVPQALLDNR-----EDECIIIS 100
 DB 73 MREPRNTHPIPRAAVYATLARKHA---GKVRDEGRVELPMLDGHANNEVEGETSEIIS 129
 OY 101 FAETGLSTINOTRLDPESSDRTAGRE--VQASL-MFVQLPSTTWTLKVRLV-- 155
 DB 130 FASBDVTPSKSLSYFLISNE---GNQNLVYLOANMLYFKLPGTLEGLAKVTVRVH 186
 OY 156 ---GPHNTNLATQVLLVEDASGWHQPLGPEAQAACSGHLLTLELVLEGQVASSV 211
 DB 187 SEPGGONVHMPM-MEVRVELKRSQWHTFRLTEPVAGVFERDRQDDVRCGEAANA 245
 OY 212 L-----GGAARPEVAARV-RVCGKHQIHRGIDCGGSRMCCROEFFVDREIGWHD 263
 DB 246 LPIIVDSDESHRPFVIVRAQADGKHRIKRLGLEDGNGGICCRQGYIDFRLIGWMD 305
 OY 264 WIDPEGAMNFCIGCPPLIAGMPCGIAASFHTAVLNLKANTAACTGG--GSCCVPA 321
 DB 306 WIIAPAGYGNVCEGSCPATVACVPSASSFHTAVVNOYRMR---GMSFQSMNSCIPTR 362
 OY 322 RRPILLSLYDRDSNVKTIDIPDMVVEACGS 352
 DB 363 LSTMSMLTFDEYNIVKRDVPMNIVECGCA 393

RESULT 6

Q9PWR8 PRELIMINARY; PRT; 392 AA.

AC Q9PWR8: 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE ACTIVIN BETA B SUBUNIT PRECURSOR.

OS Carassius auratus (Goldfish).

OC Euteleostomi; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes; Cyprinidae; Carassius.

OX NCBI_TaxID=7957;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Ovary;

RA MEDLINE=97424746; PubMed=9278859;

RT "Cloning of cDNA for goldfish activin beta B subunit, and the expression of its mRNA in gonadal and non-gonadal tissues."

RL J. Mol. Endocrinol. 19:37-45(1997).

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR EMBL: AF004669; AAB01468.1; -

DR HSSP: P12843; 3BP.

DR InterPro: IPR000381; Inhibin_betaB.

DR InterPro: IPR001318; Inhibin_betaC.

DR InterPro: IPR001839; TGF-beta.

DR InterPro: IPR001111; TGFb.N.

DR Pfam: PF000019; TGF-beta; 1.

DR Pfam: PF00668; TGFb_propeptide; 1.

DR PRINTS: PR00671; INHIBINB.

DR PRINTS: PR00672; INHIBINB.

DR PRODOM: PD000357; TGF-beta; 1.

DR SMART: SM00204; TGFb; 1.

DR PROSITE: PS00250; TGF-BETA; 1.

DR Glycoprotein: Signal.

FT SIGNAL 1 23

FT CHAIN 277 392 ACTIVIN BETA B SUBUNIT.

FT SEQUENCE 392 AA; 43853 MW; 73AA7E1C0B2450B CRC64;

Query Match 30.5%; Score 564; DB 13; Length 392;

Best Local Similarity 34.18; Pred. No. 5.1e-46;

Matches 133; Conservative 79; Mismatches 130; Indels 48; Gaps 14;

QY 1 MTSSLLAFLAPTYA--TPRAGGCPAC--GPTLEESQRELLDLAKRSLDKLHT 57

DB 13 LSVCLMACILSVGSGAETVSGESQASGLHPDSCRMOTDFEAYKRHLNLM 72

QY 58 TORFLNRPYSRALRTALQHLHGVPGALLDNR-----EDECETISF 101

DB 73 RERNITHTPIPKAMVATLRLHA--GKVEHDEGRVEIPFDGHAHNEVQEEETISIF 129

QY 102 AETGLSTINOTRLDFHFSDDTAGDRE--VOQASL-NEFVQLPS-----NTWTILKVRV 132

DB 130 AESDVTSPSSSLYFLISNE---GNOLYVLAQAMLYLFLPETOEGKLRRKYTVAVRS 166

QY 153 LVGPHNTNLTLATQVLYLEVDSGMHQLPLGPEAOAASOGHLLTLEVGVAQSSVLT 212

DB 187 YEPGQVHVHPM-MEKVEELKRSQMTFPVSEAVREKLAKGRRQDLHCEGEANVLT 245

QY 213 -----GGAHRRPVAVAR-VVGKQHIHRRGIDCCG--GSRMCCROEFVDFREIGHW 264

DB 246 PILVDPDPSHRPPLVVRADQADSKHRRGLECDTNGCLCCROOFYIDFLIGNDW 305

QY 265 IIOPEGYAMNFCIGCPPLHAGMGIAASPHAVNLNLKANTAGTTGG--GSCCVPTAR 322

DB 306 IIPAGYGVYGVGSGSCAPVAGVPGSSSHTAVVNOYRMR---GISPGVNSCCIPTKL 362

QY 323 RPLSLLYDSDSNIVKTIDPMVVEAGCGS 352

DB 363 STMSMLYDFDEYNIYKRDVPMIIVEEGCA 392

RESULT 7

Q9HBP0 PRELIMINARY; PRT; 426 AA.

AC Q9HBP0: 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE HYPOPHYSICAL 47.5 KDA PROTEIN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Plimates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,

RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,

RA Yu J., Han L.H.;

RT "Novel Human cDNA clones with function of inhibiting cancer cell growth."

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR EMBL: AF218018; AAG17260.1; -

DR HSSP: P18075; 1BP.

DR InterPro: IPR002405; Inhibin_alpha.

DR InterPro: IPR000491; Inhibin_betaA.

DR InterPro: IPR001318; Inhibin_betaC.

DR InterPro: IPR001839; TGF-beta.

DR InterPro: IPR001111; TGFb.N.

DR Pfam: PF000019; TGF-beta; 1.

DR Pfam: PF00668; TGFb_propeptide; 1.

DR PRINTS: PR00669; INHIBINA.

DR PRINTS: PR00670; INHIBINB.

DR PRINTS: PR00672; INHIBINB.

DR PRODOM: PD000357; TGF-beta; 1.

DR SMART: SM00204; TGFb; 1.

DR PROSITE: PS00250; TGF-BETA; 1.

DR Glycoprotein: Hypothetical protein.

FT SEQUENCE 426 AA; 47454 MW; 339276317BD5d408 CRC64;

Query Match 30.0%; Score 554; DB 4; Length 426;

Best Local Similarity 31.5%; Pred. No. 5.3e-45;

Matches 133; Conservative 74; Mismatches 135; Indels 80; Gaps 12;

QY 6 LIAFLAPTYA--TPRAGGCPPL--ELSSQRELLDLAKRSLDKLHT 58

DB 10 LLASCMIVYRSSPTPGSGHSAAPDCPSALALAPKDVPSQPEMVEAVKHIILNMLHK 69

QY 59 QRPTLNRPYSRALRTALQHLHGVPGALLDNR-----EDECETISF 104

DB 70 KRDPVQIPVPAKALMLAIKRLHGVGKGVGEYIEDIDIRRAEMNEMLMOTSEIITFAES 129

QY 105 GLSTINOTRLDFHFSDDTAGDRE--VOQASLMEFVQLP-SNTWT-LKRYVLVLP-- 158

DB 130 GTA-----RKLHFEISKSGSDLSVERAEVWLFLKVPANRTFRKVTIRLFOQCKHPG 184

QY 159 -----NTNLTATQVLYLEVDSGMHQLPLGPEAOAASOGHLLTLEVLG 203

DB 185 SLDTGEAEVGLKGRSLLSEKVVDAKSTMTVFPVSSIQRLDQKSSLDVRLAC 244

QY 204 QVAQSS-----VILG-----GA-----AHRPF--VAVARYVGK 230

DB 245 EOCQEGASLVLLGKKKKKEEGEGKKKGAGADEKQSHRPLMLQAROSEHP 304

QY 231 HQIHRGIDCCGSRMCCROEFVDFREIGHWMTIIOBGMANFCIGCPPLHAGMPT 290

DB 305 HRRRGLECDKVKVCKCKPFVSKFDIGMNDMILAPSGYHANYCEGCSHLAGTSGS 364

QY 291 AASFHTAVNLKANTAACTGGSCCVPTARRPRLLYYDSDSNIVKTIDPMVVEAGC 350

DB 365 SLSPHSTVINHTRMGHSHFALAKSCCVPTKLRPMMLLYDDGQNTIKKDIQNMIVEEGC 424

RESULT	ENTRY	11
TITLE	S31440	#type complete
ALTERNATE_NAMES	1mb1b1n beta A chain - mouse	
ORGANISM	activin A; mesoderm-inducing factor WEHI-231	
DATE	13-Jan-1995	#sequence_revision 13-Jan-1995 #text_change 07-Jun-1996

ACCESSIONS
REFERENCE
S31440; A60087
S31439
S31438

#submission	submitted to the EMBL Data Library, November 1992
#accession	531440

```
##molecule_type mRNA
##residues 1-424 ##label ALB
##sequence mm: 250610
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REFERENCE	Authors
A60087	Albano, R.M.; Godsave, S.F.; Huylebroeck, D.; Van Nimmen, K.

#Journal #title	Development (1990) 110:435-443 A mesoderm-inducing factor produced by WEHI-3 murine
--------------------	--

#cross-references MUID:92155098
#accession A60087

```

#residues      309-311, 'X', 313-318, 'XX', 321-325 #label AL2
CLASSIFICATION #superfamily Inhibin

```

Query Match	21.3%	Score 543	DB 6	Length 424
-------------	-------	-----------	------	------------

Matches	66;	Conservative	30;	Mismatches	41;	Indels	2;	Gaps	2.
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216 AHRPVARVRVGGRH-QIHRR-GIDCGGSRNCRQEFYDEREIGHDMIIQDEGYAM 273

```
Db      346  nycgecpcshlaqtgsssisfhtcvlnhyrmrgshpanlksccvptllrpsmamllyddg 405
```

Db 406 qnllkkdigmntveecgcs 424

QY 334 SNIVRTDIPDMVEACGS 352

RESULT ENTRY	12
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ALTERNATE_NAMES	ORGANISM
activin: mesoderm inducing factor	
#formal_name Bos primigenius taurus	#common_name cattle

DATE 01-Aug-1993 *Sequence Revision 01-Sep-1993 *Exec-Changes
25-May-1996
ACCESSIONS S50898; B25732; A60960; B61548

REFERENCE	53089/
Authors	Thompson, D.A.; Cronin, C.N.; Martin, F.
Journal	Eur. J. Biochem. (1994) 226:751-764

Genomic Cloning and Sequence Analyses of the Coding Region of Transcription Factor AP-2-Binding Sites in the beta(A)- and beta(B)-inhibin/activin genes. Identification

Accession	Status	Preliminary
S50898		

##molecule_cype DNA

```
##residues      1-425 ##label THO
##cross-references EMBL:U16238
REFERENCE      A94097
AUTHOR      Forde R C , Bird T
```

Cobon, G.S.; Gregson, R.P.; Robertson, D.M.; Morgan, F.J.; Hearn, M.T.W.; Findlay, J.K.; Wettenhall, R.E.H.; Burger, H.C.; De Grooter, D.M.

#Journal #title	Proc. Natl. Acad. Sci. U.S.A. (1986) 83:3091-3095
Cloning and sequence analysis of cDNA species coding for the two subunits of inhibitor from bovine follicular fluid	

*cross-references MUID: 86205842
#accession B25732

258-425 #label FOR
part of this sequence, including the amino end of the
#residues
#note
#note

REFERENCE
A60960
Chertov, O.Y.; Krasnosel'skiĭ, A.L.; Bogdanov, M.E.;
Chertov, O.Y. *Tr. Vsesoyuzn. nauch. issled. inst. matemat. mekhan.* 1978, 10, 1, 1-10.

#Journal #title	Blomed. Sci. (1990) 1:499-506
Mesoderm-inducing factor from bovine amniotic fluid	
Identification and N-terminal amino acid sequence	

determination.
#accession A60960

```

#residues      310-312, 'X', 314-319, 'XX', 322-328, 'P' ##label CHE
REFERENCE      A61548

```

M.; Kangawa, K.; Matsuo, H.
Mol. Cell. Endocrinol. (1986) 44:55-60

```

#accession      B61548
#molecule_type protein

```

GENETICS
#Introns 130/1

KEYWORDS disulfide bond; glycoprotein; gonad; heterodimer; homodimer hormone

```

1-28 #domain signal sequence #status predicted #label sig
29-309 #domain propeptide #status predicted #label pro\

```

```

#label MAT\
#binding_site carbohydrate (Asn) (covalent) #statun
165

```

SUMMARY

#length	425	#molecular-weight	47521	#checks	507
---------	-----	-------------------	-------	---------	-----

Best Local Similarity	47.58;	Pred. No. 1.13e-76;	
Matches	66;	Conservative	30;
		Mismatches	41;
		Indels	2;
		Gaps	2

```
Db 287 shrpflmqrsedhphrrrrglcedgkvnlcckkqfvsfkldgmdwllapsgyha 346
::|||: : | : : || |:::| :||: :||| |::|||:| | |
```

Db 347 nycgeecpshtagtcgsslsfhsstvinhyrmrghspfnlksccvptklrmmamllyddg 406

274 NFGGCELIHAGMGIASFTAVLNLKANTAGTGGSCCVTARRPLSLTYDRD 333

DB	407	qnlrkauqlmnlveecgcs	422
1/0Y	334	SNIVKTDIPDMVEACGCS	353

RESULT 13

ALTERNATE NAMES	TITLE	ENTRI
activin A; activin AB chain A; erythroid differentiation	inhibin beta-A chain precursor - human	524240
	* type complete	

	factor; megakaryocyte differentiation active protein
MANISM	
#formal_name Homo sapiens	#common_name man
21-May-1988	#sequence_revision 21-May-1988
	#text_change

OY 351 CS 352
11
DB 425 CS 426

RESULT 8
098860 PRELIMINARY: PRT: 413 AA.

AC 098860: 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ACTIVIN BETA-A SUBUNIT.
OS Cynops pyrrhogaster (Japanese common newt)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=9629508; PubMed=8702409;
RA Yamamoto T., Nakayama Y., Abe S.;
RT "Expression of activin beta subunit genes in sertoli cells of newt
testis.";
RL Biochem. Biophys. Res. Commun. 224:451-456(1996).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: D84516; BAI2693.1;
DR HSSP: P18075; 1BP.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR000491; Inhibin_betaA.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR PRINTS: PR00670; INHIBINB.
DR PRINTS: PR00672; INHIBINB.
DR PRODOM: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 413 AA: 46303 MW: 46660112AA1B010 CRC64;

Query Match 29.6%; Score 547; DB 13; Length 413;
Best local Similarity 32.3%; Pred. No. 2.4e-44;
Matches 132; Conservative 59; Mismatches 152; Indels 66; Gaps 11;

OY 5 LLAFLAAPTVAAPRAGQ-----CPACGPTLE--LESORELLDLAKRSLDKLHL 57
DB 10 LLLGLCIAIATRASPTCTEGGCVTDPCSCALGRLEKAAPSSQADNVEAYVKHLLMLHM 69
OY 58 TORPTLNRPVSRALNTALQHLH-----GYPGALLLEDN-----REGECEIISFAE 103
DB 70 RSRNITQIPVKAALNAIKKHLVGVGDGVEIEDDVGRAESELLEDTSEITTFAE 129
OY 104 TGLSTINOTRLDHFSSDRTACDRE--VQOASIMFVQLPENTTWTLKVRVVLV----- 155
DB 130 AG-----QSKVHLFEISKEGSDLSLVEQAEFLFKLMSRSRTKLTIRLYQOQORGO 184
OY 156 -----GPHNTNLATQYLLEVDASGHWLPDREPQAAACSGHLLTLELVLEGVQAASS- 209
DB 185 DEERGOERDKKEVLIAEKTLDTRKSGMHTFNIAKSIQHLDDGKTSLDRIKQDCCOCITG 244
OY 210 ---VILG-----GAA-----HRRP--VAARVVGKHIQIHRGIDCOCG 243
DB 245 ATPTLLGKKKKKEEVKAANSAGDEREGRSHRPLIMARQEEHPIHRRRRRGLECDCK 304
OY 244 SHMCCROEFVDFREIGWDMITIOPEGYAMNFCIGCCPLHIAQMPIASFPAVLNLK 303
DB 305 VSICCKQGFYVSKFDIGMSDVIAPPGTANYCGDGPMTITSSGSGFSFAAVINQVR 364
OY 304 ANTAAGTTGGGSCVTPARPLSLLYYDRDSINIVTQDIPDMVEACGCS 352
DB 365 MKGYSPFTSVKSCVPTKLRAKMSHLYDDGQNIKKDIGNMVEECGCS 413

RESULT 9
098SP9 PRELIMINARY: PRT: 424 AA.

AC 098SP9: 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE INHIBIN-BETA.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Ahn J., You S., Kim H., Foster D.N., El Halawani M.E.;
RT "Molecular cloning of turkey inhibin-alpha and beta subunits.";
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF36338; AKK21265.1;
DR HSSP: AF36338; 1BP.
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR000491; Inhibin_betaA.
DR InterPro: IPR001839; Inhibin_betaC.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR PRINTS: PR00669; INHIBINB.
DR PRINTS: PR00670; INHIBINB.
DR PRINTS: PR00672; INHIBINB.
DR PRODOM: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 424 AA: 47442 MW: B3E7CF3B9DF0C59 CRC64;

Query Match 28.8%; Score 533; DB 13; Length 424;
Best local Similarity 30.5%; Pred. No. 5.6e-43;
Matches 128; Conservative 69; Mismatches 145; Indels 78; Gaps 10;

OY 6 LLAFLAAPTVAAPRAGQ-----CPACGPTLE--LESORELLDLAKRSLDKLHL 58
DB 10 LLYICWTIVRSPTPSEGHSSVTDCPCALTTLSKDVPSQPEVNEAYVKHLLMLHLR 69
OY 59 ORPTLNRPVSRALNTALQHLH-----GYPGALLLEDN-----REGECEIISFAE 104
DB 70 DRNITQIPVKAALNAIKKHLVGVGDGVEIEDDVGRIQONNEVEQTSSEITTFROS 129
OY 105 GLSTINOTRLDHFSSDRTACDRE--VQOASIMFVQLPENTTWTLKVRVVLV----- 158
DB 130 G--TPKT--LHFEISKEGSELVEVHAFLFKVANSRRTKVTIRLFQOOROPKG 184
OY 159 -----NNTNLATQYLLEVDASGHWLPDREPQAAACSGHLLTLELVLEG 203
DB 185 NSEGESEMEDGLKGESESLISEKAVDTKSTWHLFPVSSVQRLDDGKSSLDVRIAC 244
OY 204 QVAQ-----SSVILG-----GAAHRRP--VAARVVGKHIQ 232
DB 245 DLQCTGATGLVILGKKKKKEDGKEDGKELTGEREKOSHRPLMLAHNSDROHR 304
OY 233 IHRGIDCOCGSRMCCROEFVDFREIGWDMITIOPEGYAMNFCIGCCPLHIAQMPIASF 292
DB 305 RRRKGLFCGCKYKNIKKQGFVSKFDIGMSDVIAPPGTANYCGDGPMTITSSGSGFS 364
OY 293 SPHTAVNLKNTAAGTTGGGSCVTPARPLSLLYYDRDSINIVTQDIPDMVEACGCS 352
DB 365 SEHSTVINHYRMGRGSPANLKSCTVPTKLKPMKMSHLYDDGQNIKKDIGNMVEECGCS 424

RESULT 10

09PM65
ID 09PM65 PRELIMINARY: PRT: 404 AA.
AC 09PM65:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ACTIVIN BETA A PRECURSOR.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN, PITUITARY;
RA Yam K.M., Tu K.L., Ge W.;
RT *Cloning and characterization of activin beta A subunit.*;
RL Mol. Cell. Endocrinol. 0:0-0(1999).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF169032; AAD50448.1; -.
DR HSSP: P12643; 3BMP.
DR Interpro: IPR002405; Inhibin_alpha.
DR Interpro: IPR000491; Inhibin_beta.
DR Interpro: IPR001839; TGF-beta.
DR Interpro: IPR001111; TGF-beta.
DR Pfam: PF000019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta; 1.
DR PRINTS: PR00669; INHIBIN.
DR PRINTS: PR00670; INHIBIN.
DR Prodom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-BETA; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 289 404 POTENTIAL.
SQ SEQUENCE 404 AA: 44799 MW: 34641B62AACDC CRC64;
Query Match
Best Local Similarity 28.0%; Score 518; DB 13; Length 404;
Matches 121; Conservative 68; Mismatches 127; Indels 76; Gaps 11;
OY 14 PTTVTPRAGGCGPCGPTLELSOREL-LDDAKRSIIDKHLTORPLNRPVSRAAL 72
DB 36 PDDPVT-----CPSCALAKQKQSEEDTDVEAVKRIIMLHNTLRPVHTHPRAAL 90
OY 73 RTALQHL-----GVPGALLDRECEIISFAENGSTINOTRLDHF 117
DB 91 LNAIRRLHVGAVGEDGVEMEEDGGEGEHRDSEEDPELITFAEPG-DAPDIKFDIS 149
OY 118 FSSDRTAGDREVQASIMFVQLPSNTTWLTKRYLVL-----GPHNTLTLAT 166
DB 150 MEGNTLS---VEGANWMLLKAKGKRGKVSQVLQHGKADPGSADGPOE---AVVS 203
OY 167 QYLLEVASGCHOLPLGPEAQAACSGHLLTLELVLEGQAQSSVL-----GGA---- 215
DB 204 EKYVDRSRGSMHTLPVS-----RTVQLLDGDSMLSLKVSQCMCAEAVPIL 252
OY 216 -----AHPFYAARVYRGCKHQIHR--RGIDCGSGRRCROEFFVDFREIG 260
DB 253 VPRESNKGKREDSHRPFLAVVLKPAEEHPRHRSKRGLECDCKIRVCKRGQYVFXKIG 312
OY 261 WHDMIIQPEGYANNCIGCCPLIHGMPRIASFTAVLNLKATTAAGTTGGSCCVP 320
DB 313 WSMIITAPSGYHANYCEGDCPSHVASITGSALSTFSTYINIRMGVSPFNINISCCVPT 372
OY 321 ARPLSLLYDDNSNVTKDIDPDAVVEAGCS 352
DB 373 RLRASMLTYNEOKIKIKDKIDNMTVECCGS 404
RESULT 11
09DGE9 PRELIMINARY: PRT: 115 AA.
ID 09DGE9

AC 09DGE9:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INHIBIN/ACTIVIN (FRAGMENT).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC Tada T., Hiroo I., Aoki T., Takashima F.;
RT *Cloning and sequencing of carp and medaka activin subunit genes.*;
RL Fisheries Sci. 64:680-685(2000).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AB009406; BAB1759.1; -.
DR HSSP: P12643; 3BMP.
DR Interpro: IPR002405; Inhibin_alpha.
DR Interpro: IPR001839; TGF-beta.
DR Pfam: PF000019; TGF-beta; 1.
DR PRINTS: PR00669; INHIBIN.
DR Prodom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-BETA; 1.
KW Glycoprotein.
FT NON_TER 1 115
FT NON_TER 1 115
SQ SEQUENCE 115 AA: 12666 MW: CD38FA0DD7BD52A6 CRC64;
Query Match
Best Local Similarity 19.1%; Score 354; DB 13; Length 115;
Matches 61; Conservative 23; Mismatches 28; Indels 6; Gaps 3;
OY 237 GUIDCGG-GRMCCROEFFVDFREIGMHDMIIQPEGYANNCIGCCPLIHGMPRIASFT 295
DB 1 GLECDGTGKGLCCRQGFVDFRLGMDMIIAPAGYIGNCESSCPAYLAGVGSASSFH 60
OY 296 TAVLMLKANTNAAGTTG--GSCVPTARRPLSLYYDRDSNIVKTDIDPDAVVEAGC 351
DB 61 TAVVQYRMR--GMSPSVNSCIPKLTSMWLFVDEDEYNIVKRDVNMIVRECCG 115
RESULT 12
095KPI PRELIMINARY: PRT: 119 AA.
ID 095KPI
AC 095KPI:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ACTIVIN SUBUNIT A (FRAGMENT).
OS Alluvius fulgens (Lesser panda).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Alluvius.
OX NCBI_TaxID=9649;
RN [1]
RP SEQUENCE FROM N.A.
RC Wang X., Wang Y.;
RT *Molecular cloning of the activin gene A subunit mature peptide from
RT panda related animals.*;
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY025555; AAK40342.1; -.
FT NON_TER 1 119
FT NON_TER 1 119
SQ SEQUENCE 119 AA: 13328 MW: 0A319B2F25D83C66 CRC64;
Query Match
Best Local Similarity 19.1%; Score 354; DB 6; Length 119;
Matches 58; Conservative 21; Mismatches 36; Indels 0; Gaps 0;
OY 237 GUIDCGG-GRMCCROEFFVDFREIGMHDMIIQPEGYANNCIGCCPLIHGMPRIASFT 296
DB 3 GLECDGVNICKKQKQFVSEFKIDGMNDMIIAPSGYHANYCEGDCPSHIVKGTSSSLFS 62

OY 297 AVNLKANTAGTGGSCVPTARRPLSLYYDRDSNIYKTDIPDMVVEACGC 351
 DB 63 TVINNH RMGRSPFANLKSVCVPTKLRPMMLYDDGONIKKIDIONMIVECCG 117

RESULT 13

O42125 PRELIMINARY; PRT: 119 AA.

ID 042125
 AC 042125: 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE ACTIVIN BETA B (FRAGMENT).
 OS Pagrus major (Red sea bream) (Chrysophrys major).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
 CC Sparidae; Pagrus.
 NCBI_TaxID=143350;
 OX NCBI_TaxID=143350;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OVERLY;
 RA Sakakida Y., Kasahara M., Inaba K.;
 RT "Analysis of the actin beta B subunit of Pagrus major."
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC HSSP: AB006786; BAA22570.1; -.
 DR EMBL: AB006786; BAA22570.1; -.
 DR InterPro: IPR001839; TGF-beta.
 DR Pfam: PF00019; TGF-beta; 1.
 DR ProDom: PD000357; TGF-beta; 1.
 DR SMART: SM00204; TGF-beta; 1.
 DR PROSITE: PS00250; TGF-BETA; 1.
 KW Glycoprotein.
 FT NON_TER 1
 FT NON_TER 119
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13455 MW; EFB0E9E9AD1FA888 CRC64;

Query Match 19.1%; Score 353.5; DB 13; Length 119;
 Best Local Similarity 52.2%; Pred. No. 2.4e-26;
 Matches 60; Conservative 23; Mismatches 27; Indels 5; Gaps 2;

OY 230 KQIHRRGIDCGGSMCCROEFVDFRIGMHWIIOPEGYAMNFCIGCCPLHAGMG 289
 DB 8 KHRIRKGLCCDSSSLCCROQFYIDFRIGMNDWIIAPSGIFGVGSCGCPATMAGVPG 67
 OY 290 IASFTAVNLKANTAGTGG--GSCVPTARRPLSLYYDRDSNIYKTDIP 342
 DB 68 SASSFTAVVNOYRMR---GMSFGSNSSCIPFKLSTMSMLYFDDEYNIVKRDVP 119

RESULT 14

O9DGE1 PRELIMINARY; PRT: 115 AA.

ID 09DGE1
 AC 09DGE1: 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE INHIBIN/ACTIVIN (FRAGMENT).
 OS Cyprinus carpio (Common carp).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 CC Cypriniformes; Cyprinidae; Cyprinus.
 NCBI_TaxID=7962;
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tada T., Hirono I., Aoki T., Takashima F.;
 RT "Cloning and sequencing of carp and medaka activin subunit genes."
 RL Fisheries Sci. 64:680-685(2000).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL: AB009404; BAB17597.1; -.
 DR HSSP: P12643; 3BMP.

DR InterPro: IPR002405; Inhibin_alpha.
 DR InterPro: IPR001839; TGF-beta.
 DR Pfam: PF00019; TGF-beta; 1.
 DR PRINTS: PR00669; INHIBIN.
 DR ProDom: PD000357; TGF-beta; 1.
 DR SMART: SM00204; TGF-beta; 1.
 DR PROSITE: PS00250; TGF-BETA; 1.
 KW Glycoprotein.
 FT NON_TER 1
 FT NON_TER 115
 FT NON_TER 115
 SQ SEQUENCE 115 AA; 12684 MW; CD38FBBC67BCE316 CRC64;

Query Match 19.1%; Score 353; DB 13; Length 115;
 Best Local Similarity 51.7%; Pred. No. 2.4e-26;
 Matches 61; Conservative 23; Mismatches 28; Indels 6; Gaps 3;

OY 237 GIDCG-GSRMCCROEFVDFRIGMHWIIOPEGYAMNFCIGCCPLHAGMGIAASPH 295
 DB 1 GLECDGTNGGLCCROQFYIDFRIGMNDWIIAPAGYGVNCEGSCPAVYAGVGSASSPH 60
 OY 296 TAVNLKANTAGTGG--GSCVPTARRPLSLYYDRDSNIYKTDIPDMVVEACGC 351
 DB 61 TAVVNOYRMR---GMSFGSNSSCIPFKLSTMSMLYFDDEYNIVKRDVPNMIYEECCG 115

RESULT 15

O9DGE6 PRELIMINARY; PRT: 115 AA.

ID 09DGE6
 AC 09DGE6: 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE INHIBIN/ACTIVIN (FRAGMENT).
 OS Oryzias latipes (Medaka fish).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Percomorpha; Athieriomorpha;
 CC Belontiiformes; Adiantichthyidae; Oryziinae; Oryzias.
 NCBI_TaxID=8090;
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tada T., Hirono I., Aoki T., Takashima F.;
 RT "Cloning and sequencing of carp and medaka activin subunit genes."
 RL Fisheries Sci. 64:680-685(2000).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL: AB009409; BAB17602.1; -.
 DR HSSP: P12643; 3BMP.
 DR InterPro: IPR002405; Inhibin_alpha.
 DR InterPro: IPR001839; TGF-beta.
 DR Pfam: PF00019; TGF-beta; 1.
 DR PRINTS: PR00669; INHIBIN.
 DR ProDom: PD000357; TGF-beta; 1.
 DR SMART: SM00204; TGF-beta; 1.
 DR PROSITE: PS00250; TGF-BETA; 1.
 KW Glycoprotein.
 FT NON_TER 1
 FT NON_TER 115
 FT NON_TER 115
 SQ SEQUENCE 115 AA; 12684 MW; CD38FBBC67BCE316 CRC64;

Query Match 19.1%; Score 353; DB 13; Length 115;
 Best Local Similarity 51.7%; Pred. No. 2.4e-26;
 Matches 61; Conservative 23; Mismatches 28; Indels 6; Gaps 3;

OY 237 GIDCG-GSRMCCROEFVDFRIGMHWIIOPEGYAMNFCIGCCPLHAGMGIAASPH 295
 DB 1 GLECDGTNGGLCCROQFYIDFRIGMNDWIIAPAGYGVNCEGSCPAVYAGVGSASSPH 60
 OY 296 TAVNLKANTAGTGG--GSCVPTARRPLSLYYDRDSNIYKTDIPDMVVEACGC 351
 DB 61 TAVVNOYRMR---GMSFGSNSSCIPFKLSTMSMLYFDDEYNIVKRDVPNMIYEECCG 115

Tue Oct 15 13:49:41 2002

Job time : 45 secs

us-09-684-383-2.rspt

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2002, 22:05:48 ; Search time 1932.25 seconds
(without alignments)
16873.397 Million cell updates/sec

Title: US-09-684-383-3

Perfect score: 1558

Sequence: 1 AAGAGTCATGCCAGTCGGA.....ATGCCCTAGTCTCTCCCTT 1558

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: gb-ha:*
2: gb-hcg:*
3: gb-ln:*
4: gb-om:*
5: gb-ov:*
6: gb-pat:*
7: gb-pn:*
8: gb-pl:*
9: gb-pr:*
10: gb-ro:*
11: gb-sts:*
12: gb-sy:*
13: gb-un:*
14: gb-vl:*
15: em-da:*
16: em-fun:*
17: em-hum:*
18: em-ln:*
19: em-mu:*
20: em-om:*
21: em-or:*
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23: em-pat:*
24: em-ph:*
25: em-pl:*
26: em-ro:*
27: em-sts:*
28: em-un:*
29: em-vl:*
30: em-htg-hum:*
31: em-htg-lnv:*
32: em-htg-other:*
33: em-htgo-lnv:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Match Length DB ID Description

1	1558	100.0	1558	6	A48432	A48432 Sequence 3
2	1558	100.0	1558	6	AR038926	AR038926 Sequence
3	1558	100.0	1558	6	AR123395	AR123395 Sequence
4	1547	99.3	1565	10	MMINACTS	X90819 M.musculus
5	1471.2	94.4	1624	10	MM095962	U95962 Mus musculus
6	1105	70.9	2049	10	MMINBXC2	X90842 M.musculus
7	1037.4	66.6	2433	10	MMACTBC02	U40773 Mus musculus
8	915	58.7	1056	10	AF140031	AF140031 Rattus no
9	781	50.1	2272	6	A48430	A48430 Sequence 1
10	781	50.1	2272	6	AR038925	AR038925 Sequence
11	781	50.1	2272	6	AR123394	AR123394 Sequence
12	781	50.1	2272	6	AR137665	AR137665 Sequence
13	781	50.1	2272	6	HSACTN6C	X82540 H.sapiens m
14	778	49.9	2272	6	AX083554	AX083554 Sequence
15	778	49.9	2272	6	AX137805	AX137805 Sequence
16	555.6	35.7	168473	2	AC063917	AC063917 Homo sapi
17	550.8	35.4	181272	2	AC022506	AC022506 Homo sapi
18	524.8	33.7	185688	2	AC018805	AC018805 Homo sapi
19	436.2	28.0	920	10	MMACTBC01	U40772 Mus musculus
20	436.2	28.0	1212	10	MMINBXC1	X90841 M.musculus
21	230.4	14.8	168473	2	AC063917	AC063917 Homo sapi
22	212.2	13.6	265	6	AR137666	AR137666 Sequence
23	149.8	9.6	1859	5	XELACTID	D49543 Xenopus lae
24	145	9.3	1749	10	BC010404	BC010404 Mus muscu
25	145	9.3	2125	10	MMU96386	U96386 Mus musculus
26	143.4	9.2	687	6	E03666	E03666 DNA sequence
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28	141.8	9.1	2600	10	AF089825	AF089825 Rattus no
29	140.8	9.0	1053	10	AF140032	AF140032 Rattus no
30	137	8.8	2454	9	BC005161	BC005161 Homo sapi
31	137	8.8	191097	2	AC072033	AC072033 Homo sapi
32	136	8.7	360	6	AR052495	AR052495 Sequence
33	136	8.7	360	6	AR112341	AR112341 Sequence
34	131.2	8.4	978	9	BTB1NH2	U16211 Bos taurus
35	129.4	8.3	1737	9	HUMINHB2	M1669 Human lmb1b
36	129.4	8.3	1966	6	101852	101852 Sequence 14
37	129.4	8.3	1966	6	105284	105284 Sequence 25
38	129.4	8.3	1966	6	121915	121915 Sequence 44
39	129.4	8.3	1966	6	164621	164621 Sequence 44
40	129.4	8.3	1966	6	187903	187903 Sequence 44
41	129.4	8.3	1966	6	HUMINHBB	M13437 Human ovar1
42	129.4	8.3	217346	9	AC012363	AC012363 Homo sapi
43	128.6	8.3	2716	5	S61773	S61773 act1vln bet
44	127	8.2	1524	4	SSINHBR	X03267 Porcine mRN
45	127	8.2	1524	6	105234	105234 Sequence 16

ALIGNMENTS

RESULT 1
A48432 LOCUS A48432 1558 bp DNA Linear PAT 07-MAR-1997
DEFINITION Sequence 3 from Patent WO9601316.
A48432
VERSION A48432.1 GI:2302222
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1558)
AUTHORS Hooten G., Neidhardt H., Bechtold R. and Pohl J.
TITLE NOVEL GROWTH OR DIFFERENTIATION FACTOR OF THE TGF- beta FAMILY
JOURNAL Patent: WO 9601316-A 3 18-JAN-1996;
BIOPHARM GRS ZUR BIOTECHNOLOGI (DE)
COMMENT Other publication AU 2979895 960125
Other publication DE 19511243 960104.
FEATURES
Location/Qualifiers
1..1558
/organism="Mus musculus"
/db_xref="taxon:10090"

BASE COUNT 340 a 453 c 398 g 367 t

ORIGIN

Query Match	100.0%	Score 1558	DB 6	Length 1558
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1558; Conservative	0	Mismatches	0	Gaps 0

QY	1	AAGAGCTGATGCCAGTGCAGGAGGCTACATCAATTCCTCCCAAGGATCCCTGATGCCCCAGGAC	60
Dp	1	AAGGAGTCATATGCCATGCGAGGCTCACTCAATTCCTCCCAAGGATCCCTGATGCCCCAGGAC	60
QY	61	AGAGTTGAAGCACTCCCGTTTGAGACCCCTGAATATAGGCTTTTGATCTCTTAAAGAGGCTA	120
Dp	61	AGAGTTGAAGCACTCCCGTTTGAGACCCCTGAATATAGGCTTTTGATCTCTTAAAGAGGCTA	120
QY	121	TCCTCCAGCAATGGCTCTCTCTTGCTCCTGGCTCTTCTGTTCTGACTCCAAAGCAGT	180
Dp	121	TCCTCCAGCAATGGCTCTCTCTTGCTCCTGGCTCTTCTGTTCTGACTCCAAAGCAGT	180
QY	181	AGTAAACCCCAAAAGAGAGGCTCATGCCAGCATGTTGGGTGGCATCTTTGATCTGGA	240
Dp	181	AGTAAACCCCAAAAGAGAGGCTCATGCCAGCATGTTGGGTGGCATCTTTGATCTGGA	240
QY	241	GAGCCAGCGGAGAGCTGCTTCTCGATTTTGCCAAAGAAAGTATCCTGAGCAAGCTGCACCT	300
Dp	241	GAGCCAGCGGAGAGCTGCTTCTCGATTTTGCCAAAGAAAGTATCCTGAGCAAGCTGCACCT	300
QY	301	CAGCCAGCGGCGCCATACTCATGTGGGCAATGTCCAAAGGGGGCTCTCAAGACCGGCTGCA	360
Dp	301	CAGCCAGCGGCGCCATACTCATGTGGGCAATGTCCAAAGGGGGCTCTCAAGACCGGCTGCA	360
QY	361	CGCGCTCCGGGCGCTCGACGGGAAACCGTGTGGAGCTGACACAGAGCAAGAGATTA	420
Dp	361	CGCGCTCCGGGCGCTCGACGGGAAACCGTGTGGAGCATGACAGAGCAAGAGATTA	420
QY	421	TGAGATCATAGCTTTGCTGACACAGACCTCTTCACATCAACCAAGCCGGCTCGAGTT	480
Dp	421	TGAGATCATAGCTTTGCTGACACAGACCTCTTCACATCAACCAAGCCGGCTCGAGTT	480
QY	481	CCACTTCCTGATGAGAAATGGCCAGTGGGATGGAGGTGCGGGACCGCTTCATCTTCTT	540
Dp	481	CCACTTCCTGATGAGAAATGGCCAGTGGGATGGAGGTGCGGGACCGCTTCATCTTCTT	540
QY	541	CGTGCACTTCCCGCCACAAATGCCAACCCAGACATATMAAGTTCCTTGCTAAAGCC	600
Dp	541	CGTGCACTTCCCGCCACAAATGCCAACCCAGACATATMAAGTTCCTTGCTAAAGCC	600
QY	601	ATATGACACCAACCTCACTTGACAAGTCAATGCTGTGTCAGGTGAATGCCATGCTG	660
Dp	601	ATATGACACCAACCTCACTTGACAAGTCAATGCTGTGTCAGGTGAATGCCATGCTG	660
QY	661	GTACACACTTCTCCTGGAGCTGAAGCTGAAGTGTTCACGCCAGGGACACTTACTCT	720
Dp	661	GTACACACTTCTCCTGGAGCTGAAGCTGAAGTGTTCACGCCAGGGACACTTACTCT	720
QY	721	GGAGCTGTATACAGAAAGCCAGGTGGCCACAAAGTTCCTGATCTGGGCTGGTTTTCCCA	780
Dp	721	GGAGCTGTATACAGAAAGCCAGGTGGCCACAAAGTTCCTGATCTGGGCTGGTTTTCCCA	780
QY	781	CAGGCCCTTTTGTGGCAGCCAGGTAAAGGGTGTGAGGCAAGCATCGGGTTCCGCGCGAGG	840
Dp	781	CAGGCCCTTTTGTGGCAGCCAGGTAAAGGGTGTGAGGCAAGCATCGGGTTCCGCGCGAGG	840
QY	841	TATGATTTGCCAGAGGGGCTCGAGATGTGTCTCGACAAAGATTTTTTTGTATGACTTCCG	900
Dp	841	TATGATTTGCCAGAGGGGCTCGAGATGTGTCTCGACAAAGATTTTTTTGTATGACTTCCG	900
QY	901	TGAGATTTGGCTGGAATGACTGATCATCCAGCCTGAAGGCTATGCCATGAACCTTCTGCAC	960
Dp	901	TGAGATTTGGCTGGAATGACTGATCATCCAGCCTGAAGGCTATGCCATGAACCTTCTGCAC	960
QY	961	TGGGCAATGCCCACTACATGTGGCAGGCAATGCCCTGGCATCTCTGGCTCCTTTCACACATGC	1020
Dp	961	TGGGCAATGCCCACTACATGTGGCAGGCAATGCCCTGGCATCTCTGGCTCCTTTCACACATGC	1020

QY	1021	AGTGTGATATCGCTCCAAAGCCACACGACGCTGTGGACACATGGCAGAGGGCTGTGGTG	1080
Db	1021	ACTGCTGATATCGCTCCAAAGCCACGACGCTGTGGACACACTGGCAGAGGGCTGTGGTG	1080
QY	1081	CGTGCCTACATCTCGGGCCCTCTGTCTTTGGCTACTATGACAGGAGCAGACATTTGT	1140
Db	1081	CGTGCCTACATCTCGGGCCCTCTGTCTTTGGCTACTATGACAGGAGCAGACATTTGT	1140
QY	1141	CAAGACGGATTTACCTGACATGTTGGTGAGGCCGCGGGGTGTACTTGAATATGAGGTGA	1200
Db	1141	CAGACGGATTTACCTGACATGTTGGTGAGGCCCTCGCGGGTGTACTTGAATATGAGGTGA	1200
QY	1201	TACAGGCTGCCGTGAGGTAGAAATGGCCTTCTCAGAGAGGAAACTGTCTCCACTTTGTG	1260
Db	1201	TACAGGCTGCCGTGAGGTAGAAATGGCCTTCTCAGAGAGGAAACTGTCTCCACTTTGTG	1260
QY	1261	TCCAAATGSGAAACACTTTTTCBAACATGACGACATCCCTCTGTGTGACTTCAGGGGAAATCC	1320
Db	1261	TCCAAATGSGAAACACTTTTTCBAACATGACGACATCCCTCTGTGTGACTTCAGGGGAAATCC	1320
QY	1321	ACCTCTAAAGAGAGACACTAGTGACCAACAGCCTTTCCTCTCCCTGCGGAGCATGTTGACC	1380
Db	1321	ACCTCTAAAGAGAGACACTAGTGACCAACAGCCTTTCCTCTCCCTGCGGAGCATGTTGACC	1380
QY	1381	CAGTACACCCATCCTTCACACCTTAAATGTAGAGGCTTAAATGGACCTCCACATATATATGTCAT	1440
Db	1381	CAGTACACCCATCCTTCACACCTTAAATGTAGAGGCTTAAATGGACCTCCACATATATATGTCAT	1440
QY	1441	TTTGTCTAGCAAAACACCCCTTAGTCCCCCTTAGTCACTATGTAATCTACTCTGACCTCC	1500
Db	1441	TTTGTCTAGCAAAACACCCCTTAGTCCCCCTTAGTCACTATGTAATCTACTCTGACCTCC	1500
QY	1501	CTGACCCCTGCCACCGGAGATTTCCATATTCACAGATGATATGCTCTAATGTCCTCCCTT	1558
Db	1501	CTGACCCCTGCCACCGGAGATTTCCATATTCACAGATGATATGCTCTAATGTCCTCCCTT	1558

RESULT 2									
AR038926									
LOCUS	AR038926		1558 bp	DNA					linear
DEFINITION	Sequence 3 from patent US 5807713.								PAT 29-SEP-1999
ACCESSION	AR038926								
VERSION	AR038926..1		GI:5958289						
KEYWORDS	.								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	Unclassified.								
AUTHORS	I (bases 1 to 1558)								
TITLE	Hotten,G., Neidhardt,H., Bechtold,R. and Pohl,J.								
JOURNAL	DNA encoding growth/differentiation factor								
FEATURES	Patent: US 5807713-A 3 15-SEP-1998;								
SOURCE	location/Qualifiers								
	1..1558								
	/organism='unknown'								
BASE COUNT	340 a	453 c	398 g	367 t					
ORIGIN									

Query Match	100.0%	Score 1558	DB 6	Length 1558
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1558	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	1	AAGAGGTATCTCCAGTGCAGAGTCAAGTACATTTCTCCACAGGTCCTCGGAGCCACAGAC	60
QY	1	AAGAGGTATCTCCAGTGCAGAGTCAAGTACATTTCTCCACAGGTCCTCGGAGCCACAGAC <td>60</td>	60
Db	1	AAGAGGTATCTCCAGTGCAGAGTCAAGTACATTTCTCCACAGGTCCTCGGAGCCACAGAC	60
QY	61	AGAGTTGAAGCAGTCGCCGTTGAGACCCCTGAAATATAGCTTTGGGTCCCTTAAAGAGGCTA	120
Db	61	AGAGTTGAAGCAGTCGCCGTTGAGACCCCTGAAATATAGCTTTGGGTCCCTTAAAGAGGCTA	120
QY	121	TCTCTCAGCAATGGGCTCTCTCTTGCCTTCAGGCTTCCTGTGTCGACTCCCAACACAGT	180
Db	121	TCTCTCAGCAATGGGCTCTCTCTTGCCTTCAGGCTTCCTGTGTCGACTCCCAACACAGT	180

QY	181	AGTGAACCCCAAACTAGAGGGTCCATGCGCCAGCATGTTGGGGTGGCACTCTTGAACCTGG	240
DB	181	AGTGAACCCCAAACTAGAGGGTCCATGCGCCAGCATGTTGGGGTGGCACTCTTGAACCTGG	240
QY	241	GAGCGAGCGGAGGCTGCTCTCGATTGTTGGCCAAAGAAAGTATCTCTTGAGCAAGCTGACCT	300
DB	241	GAGCGAGCGGAGGCTGCTCTCGATTGTTGGCCAAAGAAAGTATCTCTTGAGCAAGCTGACCT	300
QY	301	CAGCGAGCGGCCCATACTGATCGGCCAGTGTCCAGAGGGGGCTCTCAAGACCGGGCTGCA	360
DB	301	CAGCGAGCGGCCCATACTGATCGGCCAGTGTCCAGAGGGGGCTCTCAAGACCGGGCTGCA	360
QY	361	CGCGCTCCGGGGGCGCTCGACGGGAAACCCTGTTGGACATGACAGAGCAAGAAAGATA	420
DB	361	CGCGCTCCGGGGGCGCTCGACGGGAAACCCTGTTGGACATGACAGAGCAAGAAAGATA	420
QY	421	TGAGATCATGAGTTTGCTGACACAGACTCTCCAGCATCAACAGACCCGGCTGAGTT	480
DB	421	TGAGATCATGAGTTTGCTGACACAGACTCTCCAGCATCAACAGACCCGGCTGAGTT	480
QY	481	CCACTTCTCTGTGATGAATGGCCAGTGGCATGGAGGTCCGGAGACCGCGCTCATGTTCT	540
DB	481	CCACTTCTCTGTGATGAATGGCCAGTGGCATGGAGGTCCGGAGACCGCGCTCATGTTCT	540
QY	541	CGTGCAGTTCCCCACAAATGCGACCCAGCCAGCATGAAATTAAGAGTTCTTGCTAAGAC	600
DB	541	CGTGCAGTTCCCCACAAATGCGACCCAGCCAGCATGAAATTAAGAGTTCTTGCTAAGAC	600
QY	601	ATATGACACCAACTCACCCTTGACAAAGTATGATGCTGGTGGAGTGAATCCAGTGGCTG	660
DB	601	ATATGACACCAACTCACCCTTGACAAAGTATGATGCTGGTGGAGTGAATCCAGTGGCTG	660
QY	661	GTACAGAGTTTCTCTGGAGACTGAACCTCAACCTGCTTGGCAGCCAGGAGACCTTACTCT	720
DB	661	GTACAGAGTTTCTCTGGAGACTGAACCTCAACCTGCTTGGCAGCCAGGAGACCTTACTCT	720
QY	721	GGAGCTGTACACAGAAAGCCAGGTGGCCACAGTTCCTTGATCCTGGGGTGGTTTCCCA	780
DB	721	GGAGCTGTACACAGAAAGCCAGGTGGCCACAGTTCCTTGATCCTGGGGTGGTTTCCCA	780
QY	781	CAGGCTTTTGGGAGCGCCAGGTAAGGGGTGAAGGCAAGCATCGGGTTCCCGCGCGAGG	840
DB	781	CAGGCTTTTGGGAGCGCCAGGTAAGGGGTGAAGGCAAGCATCGGGTTCCCGCGCGAGG	840
QY	841	TATCGATTGCCAGGGGGGGTCCAGAGATGTCTGTGCAACAAGTTTTTGTGAACTTCGG	900
DB	841	TATCGATTGCCAGGGGGGGTCCAGAGATGTCTGTGCAACAAGTTTTTGTGAACTTCGG	900
QY	901	TGAGATTTGGCTGGAATGACTGGATCATCCAGCTGAAAGGCTATGCGATGAACCTTCTGAC	960
DB	901	TGAGATTTGGCTGGAATGACTGGATCATCCAGCTGAAAGGCTATGCGATGAACCTTCTGAC	960
QY	961	TGGGAGTGGCCACTATGTCGGAGGAGCATGCTGGCATCTGTGCTCTTTCACACTGC	1020
DB	961	TGGGAGTGGCCACTATGTCGGAGGAGCATGCTGGCATCTGTGCTCTTTCACACTGC	1020
QY	1021	AGTGTGAAATTCGTCTCAAAAGCCACGACGTGGTGGACACACTGGAGGGGCTGTGCTG	1080
DB	1021	AGTGTGAAATTCGTCTCAAAAGCCACGACGTGGTGGACACACTGGAGGGGCTGTGCTG	1080
QY	1081	CGTGCATCATGTCGGGCGGCTGTCTTGTGCTTACTATGACAGGACAGCAACATGTT	1140
DB	1081	CGTGCATCATGTCGGGCGGCTGTCTTGTGCTTACTATGACAGGAGCAAGCAACATGTT	1140
QY	1141	CAAGACGATATACCTGACATGTGTGTGAGGGCTCGGGGTGATAGTTACTTATGGGTGA	1200
DB	1141	CAAGACGATATACCTGACATGTGTGTGAGGGCTCGGGGTGATAGTTACTTATGGGTGA	1200
QY	1201	TACAGGCTGGCTAAGGTAAATGAGCTTCTCTCAGGAAGGGGAAACTGTGTTCCACTTCTG	1260
DB	1201	TACAGGCTGGCTAAGGTAAATGAGCTTCTCTCAGGAAGGGGAAACTGTGTTCCACTTCTG	1260

Qy	1261	TCGAGATGAAACACCTTTC	TAAAGCATGGAGACATCCCTG	TSAGACTTGAGGGATTC	1320
Qy <td>1261 <td>TCGAGATGAAACACCTTTC <td>TAAAGCATGGAGACATCCCTG <td>TSAGACTTGAGGGATTC <td>1320</td> </td></td></td></td>	1261 <td>TCGAGATGAAACACCTTTC <td>TAAAGCATGGAGACATCCCTG <td>TSAGACTTGAGGGATTC <td>1320</td> </td></td></td>	TCGAGATGAAACACCTTTC <td>TAAAGCATGGAGACATCCCTG <td>TSAGACTTGAGGGATTC <td>1320</td> </td></td>	TAAAGCATGGAGACATCCCTG <td>TSAGACTTGAGGGATTC <td>1320</td> </td>	TSAGACTTGAGGGATTC <td>1320</td>	1320
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Qy <td>1501 <td>CTGACCGCTGACCCGGAAGGTTCT <td>CAATTCACAGATGATATGCTTA <td>GTCTGCCCTT</td> <td>1558</td> </td></td></td>	1501 <td>CTGACCGCTGACCCGGAAGGTTCT <td>CAATTCACAGATGATATGCTTA <td>GTCTGCCCTT</td> <td>1558</td> </td></td>	CTGACCGCTGACCCGGAAGGTTCT <td>CAATTCACAGATGATATGCTTA <td>GTCTGCCCTT</td> <td>1558</td> </td>	CAATTCACAGATGATATGCTTA <td>GTCTGCCCTT</td> <td>1558</td>	GTCTGCCCTT	1558
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RESULT 3	ARI23395	1558 bp	DNA	linear	PAT 16-MAY-2001
LOCUS	ARI23395				
DEFINITION	Sequence 3 from patent US 617584.				
ACCESSION	ARI23395				
VERSION	ARI23395.1	GI:14108756			
KEYWORDS					
SOURCE	Unknown.				

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
1 (bases 1 to 1558)	Hotten,G., Meldhardt,H., Bechtold,R., Pohl,J. and Paulista,M.	Method of treatment with growth/differentiation factors of the TGF- β family	Patent: US 6171584-A 3 09-JAN-2001;	Location/Qualifiers

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BASE COUNT  340 a    453 c    398 g
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			Indels	0;
			Gaps	0;

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Db 1 AAGAGTCATGCCAGTCCGAGGTCAGTCACATTCCTCCAGGGTCTCCGTCGCCAGGAC 60

Qy 61 AGAGTTGAGACACTCCCGTTGAGACCCCTAATATAGCTTTGGGTCCTTTAAGGAGGCTA 120
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OY 181 AGTGAACCCCAAACTGAGGGTCATGCCAGCATTTGGGGGCGCCATTTTGACCTGGA 24
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OY |||||
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Db |||||

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07 361 GGGCCGCCCGGGGCTCGAGCGAACCCTTTGGAGCATGACCAGAGACAGACAGACAGATA 42

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Db 541 CGTGCAGTCCCGCCCAATGGCCACCCACCATGATATTAAGAGTCTTGTCTAAGACC 600
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DEFINITION M.musculus mRNA for inhibin/activin bc subunit.
ACCESSION X90819.1
VERSION    X90819.1 GI:1150508
KEYWORDS   Inhbc gene; inhibin/activin bc subunit.
SOURCE     house mouse.
ORGANISM   Mus musculus

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REFERENCE
1 (bases 1 to 1565)
Schmiltz, J., Holten, G., Jenkins, N.A., Gilbert, D.J., Copeland, N.G.,
Pohl, J. and Schrewe, H.
Structure, chromosomal localization, and expression analysis of the
mouse inhibin/activin beta C (inhbc) gene
Genomics 32 (3), 358-366 (1996)
2 (bases 1 to 1565)
Schrewe, H.
Direct Submission
Submitted (15-AUG-1995) H. Schrewe, Max-Planck-Institut fuer
Immunbiologie, Postfach 1169, D-79011 Freiburg, FRG
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Best Local Similarity 99.9% Pred. No. 0;
Matches 1558; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DEFINITION	M.musculus inbdc gene, exon 2.			
ACCESSION	X90842			
VERSION	X90842.1	GI:1150507		
KEYWORDS	inbdc gene; Inhibin; inhibin/activin bc subunit.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.			
AUTHORS	1 (bases 1 to 2049)			
TITLE	Schrewe,H.			
JOURNAL	Direct Submission			
REFERENCE	Submitted (16-AUG-1995) H. Schrewe, Max-Planck-Institut fuer Immunbiologie, Postfach 1169, D-79011 Freiburg, FRG			
FEATURES	2 (bases 1 to 2049)			
TITLE	Schmitt,J., Hotten,G., Jenkins,N.A., Gilbert,D.J., Copeland,N.G., Pohl,J. and Schrewe,H.			
JOURNAL	Structure, chromosomal localization, and expression analysis of the mouse Inhibin/activin beta C (Inbdc) gene			
MEDLINE	Genomics 32 (3), 358-366 (1996)			
FEATURES	96435913			
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3'UTR 1007..2049
BASE COUNT 471 a 538 c 500 g 540 t
ORIGIN

Query Match 70.9% Score 1105; DB 10; Length 2049;
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Matches 1116; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DB ACAGTCACTAGCTGCTGAGTGAATGCCAGTGGCTGTACACAGCTTCTCTGGACCT 499

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VERSION U40773.1 GI:1353649
KEYWORDS
SEGMENT
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 2433)
AUTHORS Lau, A.L., Nishimori, K. and Matsuzaki, M.M.
TITLE Structural analysis of the mouse act1vln beta C gene
JOURNAL Blochim. Biophys. Acta 1307 (2), 145-148 (1996)
MEDLINE 96283807
REFERENCE 2 (bases 1 to 2433)
AUTHORS Lau, A.L.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1995) Anthony L. Lau, Pathology, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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VERSION				
KEYWORDS	AR038925.1	GI:5958288		
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	REFERENCE	Unclassified. 1 (bases 1 to 2272)				
	AUTHORS	Hotten,G., Neidhardt,H., Bechtold,R., Pohl,J. and Paulista,M.				
	TITLE	Method of treatment with growth/differentiation factors of the TGF-beta family				
JOURNAL	FEATURES	Patent: US 6171384-A 1 09-JAN-2001;				
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ACCESSION AX083554
VERSION AX083554.1 GI:13185364
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SOURCE human.
ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 2272)
AUTHORS Hooten,G., Hechtold,R. and Pohl,J.
TITLE Monomeric protein of the tgf- $\beta$ (b) family
JOURNAL Patent: WO 011041-A 3 15-FEB-2001;
Hygene AG (CH)
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Matches 936; Conservative 0; Mismatches 238; Indels 7; Gaps 3;

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 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
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 AUTHORS Monomeric protein of the TGF-beta family
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 JOURNAL Hygiene AG (CH)
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GenCore version 5.1.3
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Searched: 1736436 seqs, 858457221 residues

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2	1025.4	65.8	10708 19 AAV69286	Sequence of mouse
3	779.4	50.0	2272 17 AAT71104	Transforming growt
4	778	49.9	2272 22 AAF74421	Human TGF-beta Mpi
5	212.2	13.6	265 14 AAQ47710	TGF-beta-like clon
6	169.2	10.9	5099 19 AAV38239	Nucleotide sequenc
7	145	9.3	2125 19 AAV38238	Murine liver activ
8	143.4	9.2	687 12 AAO10891	Encodes Xenopus Bo
9	137	8.8	22 AAK94607	Human full-length

10	137	8.8	2419 17 AAT16883	Human growth diffe
11	135.4	8.7	1760 19 AAV38240	Human liver activ1
12	129.4	8.3	1966 8 AAN70316	Sequence encoding
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17	116.4	7.5	14416 22 AAL05491	Human reproductive
18	116.2	7.5	425 7 AAN60429	Sequence encoding
19	116.2	7.5	958 7 AAN60427	Sequence encoding
20	115.8	7.4	1630 8 AAN70315	Sequence encoding
21	115.8	7.4	1873 11 AAQ01648	Buf-3 gene for hum
22	97.6	6.3	391 22 ABA08456	Human growth diffe
23	93.4	6.0	1667 12 AAO10890	Encodes Xenopus Bo
24	74.6	4.8	8513 22 AAS45354	Chemically pretrea
25	74.6	4.8	8513 22 AAS45367	Tumor suppressor
26	70.4	4.5	926 18 AAT90385	Human bone morphog
27	70.4	4.5	926 18 AAD18316	Human bone morphog
28	70.4	4.5	1345 16 AAO96215	Human bone morphog
29	70.4	4.5	1345 18 AAT90390	Human bone morphog
30	70.4	4.5	1345 22 AAD18337	Human bone morphog
31	69.6	4.5	926 16 AAO96207	Bone morphogenetic
32	68.2	4.4	420 19 AAV24028	Human BMP-8 gene.
33	68.2	4.4	1002 14 AAO41296	Human osteogenic p
34	68.2	4.4	1723 13 AAO28737	Sequence encoding
35	68.2	4.4	1723 14 AAO53155	Human osteogenic p
36	68.2	4.4	1723 14 AAO38946	hOP2 CDNA. Homo s
37	68.2	4.4	1723 15 AAO56200	hOP2 CDNA. Homo s
38	68.2	4.4	1723 15 AAO56233	hOP2-pp prepro for
39	68.2	4.4	1723 15 AAO57917	Human osteogenic p
40	68.2	4.4	1723 15 AAO67313	Human OP-2. Homo
41	68.2	4.4	1723 15 AAO45118	Human OP-2. Homo
42	68.2	4.4	1723 15 AAO45164	Human OP-2. Homo
43	68.2	4.4	1723 15 AAO72706	hOP2-pp prepro for
44	68.2	4.4	1723 17 AAT33443	Human osteogenic p
45	68.2	4.4	1723 17 AAT02600	hOP-2 CDNA. Homo

ALIGNMENTS

RESULT 1	AAV38237	standard; cDNA; 1837 BP.
AC	AAV38237:	
XX		
DT	01-FEB-1999	(first entry)
DE	Murine liver activin beta c polypeptide encoding cDNA.	
XX		
KW	Liver activin; beta c; beta e; cell differentiation; hematopoiesis;	
KW	erythroid; ovarian follicular maturation; hormone; neuronal survival;	
KW	spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;	
KW	osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunoassay;	
KW	menstrual disorder; transgenic; modulator; ss.	
XX		
OS	Mus sp.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	149..1207
FT		/*tag= a
FT		/product= "activin beta c polypeptide"
FT		149..208
FT	slg-peptide	/*tag= b
FT	mat-peptide	209..1204
XX		/*tag= c
PN	MO9822492-A1.	
XX		
PD	28-MAY-1998.	
XX		
PF	20-NOV-1997;	97WO-US20882.


```

OY 623 ACAAGTACGTACGTGTCAGGTGTAATGCCAGTGGTGTACACGCTTCTCTGGAGCT 682
DB 2170 ACAAGTACGTACGTGTCAGGTGTAATGCCAGTGGTGTACACGCTTCTCTGGAGCT 2229
OY 683 GAAGCTCAAGCTGCTTGCAGCCAGGACGCTTACTCTGAGAGCTGTACACGAAAGCCAG 742
DB 2230 GAAGCTCAAGCTGCTTGCAGCCAGGACGCTTACTCTGAGAGCTGTACACGAAAGCCAG 2289
OY 743 GTGGCCACAGCTTCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 802
DB 2290 GTGGCCACAGCTTCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2349
OY 803 GTAAGGCTTGAAGGCGACAGCATGCGGTTGCGCGGAGGTATGATGCGAAGGCGGCTG 862
DB 2350 GTAAGGCTTGAAGGCGACAGCATGCGGTTGCGCGGAGGTATGATGCGAAGGCGGCTG 2409
OY 863 AGGATGCTGCTGTCAGACAGAGTCTTGTAGACTTCCGTGAGTTCGCTGAGTTCGCTG 922
DB 2410 AGGATGCTGCTGTCAGACAGAGTCTTGTAGACTTCCGTGAGTTCGCTGAGTTCGCTG 2469
OY 923 ATGATTCAGACCTGAAGGCTATGCCATGAACTTTCGACAGTGGCGAGTCCGACATGAT 982
DB 2470 ATGATTCAGACCTGAAGGCTATGCCATGAACTTTCGACAGTGGCGAGTCCGACATGAT 2529
OY 983 GCAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1042
DB 2530 GCAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2589
OY 1043 AAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1102
DB 2590 AAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2649
OY 1103 CTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1162
DB 2650 CTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2709
OY 1163 GTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1222
DB 2710 GTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2769
OY 1223 GGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1281
DB 2770 GGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2829
OY 1282 TAAGCATGACAGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1341
DB 2830 TAAGCATGACAGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2889
OY 1342 TGACCAAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1401
DB 2890 TGACCAAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2949
OY 1402 TAAGTATAGAGGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1455
DB 2950 TAAGTATAGAGGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3009
OY 1456 ACCCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1515
DB 3010 ACCCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3069
OY 1516 GAAGTCTCTATTCAGAGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1558
DB 3070 GAAGTCTCTATTCAGAGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3111

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RESULT 3

AA11104

AA11104 standard; cDNA: 2272 BP.

AA11104:

09-AUG-1996 (first entry)

```

DE Transforming growth factor beta MP-121 cDNA.
XX
XX TGF-beta: MP-121; mitogen; differentiation; induction; promotion;
KW maintenance; morphogen; tissue regeneration; dental implantation;
KW wound healing; ss.
XX
XX Homo sapiens.
XX
XX Key location/Qualifiers
XX CDS 128..1186
XX FT /tag= a
XX FT /product= TGF-beta_MP-121
XX FT mat_peptide 836..1183
XX FT /tag= b
XX
XX DE19511243-A1.
XX
XX PD 04-JAN-1996.
XX
XX PF 27-MAR-1995; 95DE-1011243.
XX
XX PR 01-JUL-1994; 94DE-1423190.
XX
XX PA (BIOP-) BIOPHARM GBS BIOTECHNOLOGISCHEN ENTWICKL.
XX
XX PI Bechtold R, Neidhardt H, Pohl J, Hoelten G;
XX
XX WP1: 1996-050788/06.
XX
XX DR P-PSDB: AAR89729.
XX
XX PT DNA encoding transforming growth factor beta MP-121 - has mitogenic
XX PS and differentiation-inducing activity, e.g. for use in wound healing
XX
XX Claim 1; Page 10; 15pp; German.
XX
XX CC A cDNA library prepared using total RNA from human liver was
XX CC subjected to PCR amplification using primers corresp. to conserved
XX CC regions within the TGF-beta family. Amplification products were
XX CC subcloned and sequenced; one clone (designated pSK-MP121) was found
XX CC to contain a new sequence. Part of the insert from this clone was
XX CC used to re-screen the human liver cDNA library and a 2272 bp fragment
XX CC (i.e. the present sequence) coding for a TGF-beta-like protein was
XX CC isolated. The protein encoded by the cDNA insert has mitogenic and
XX CC differentiation-inducing properties making it (or fusion proteins
XX CC comprising it or heterodimers of the protein with a cysteine knot
XX CC motif protein) useful for inducing tissue regeneration.
XX
XX SO Sequence 2272 BP; 510 A; 663 C; 513 G; 586 T; 0 other;

```

Query Match 50.0%; Score 779.4; DB 17; Length 2272;
 Best local similarity 79.8%; Pred. No. 3.2e-218;
 Matches 958; Conservative 0; Mismatches 236; Indels 7; Gaps 3;

```

OY 28 CACATTCCTCCAGAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 86
DB 24 CACATTCCTCCAGAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 83
OY 87 CTGAATATAGAGCTTGGGCTGCTTAAAGAGGCTATGCTCAAGCAATGAGCTTCTCTTC 146
DB 84 CTGAGCCCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 143
OY 147 TCTTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 206
DB 144 TCTTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203
OY 207 GCGCCAGATGTTGGGGTCCCATCTTTTACCTGAGAGAGCCAGCGGAGCTGCTTCTGAT 266
DB 204 GTCCAGCATGTGGGGGGCCACCTTGGAGCTGAGAGCCAGCGGAGCTGCTTCTGATC 263
OY 267 TGCCCAAGAAAGTATCTGCTGACAGAGCTGACAGCCAGCGGCGCCATATGACAGTGC 326
DB 264 TGCCCAAGAGAGCATCTTGACAGAGCTGACAGCTTCAACCCAGCGGCCCAAGACTGAACGCC 323

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Db 24 CACATCTTCCAGGGGCTCTGCGAGCCAGAGAGATTGAGACACAGCTTTGAGACC 83
Oy 87 CTGATATAGAGGCTTTGGGTCCTTTAAGAGGCTATCTCCAGCAATGGCTCTCTTC 146
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84 CTGAGGCGGAGCTGTGTATGTCTCAAGAGGGGCTTCCCGAGCAATGACCTCCATATG 143
Oy 147 TCTGGCTCTTCTGTCTGACTCCAGACAGTATGTAACCCCAAACTGAGGTCAT 206
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 144 TTCTGGCTCTTCTCTCTGCTCCAGACAGTGGCCACTCCAGAGCTGGGCTCACT 203
Oy 207 GCCCAGCATGTGGGGTGGCTTGAACCTGGAGAGCCAGCGGAGCTGCTTCGATT 266
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 204 GTCCAGCAGTGTGGGGGCGCCACCTTGGAACTGGAGAGCCAGCGGAGCTCTCTTATC 263
Oy 267 TGGCCAGAGAAAGTATCTGTGAGCAAGCTGCACTCAGCAGCGGCGCCATCTAGTCGG 326
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 264 TGGCCAGAGAGATCTTGGACAAAGTGCACCTCAGCAGCGGCGCCAACTGAACTGCC 323
Oy 327 CAGTGTCCAGAGGGGCTCTCAAGACCGGCTGCGAGCGCTCCGCGGCTCGAGCGGAAA 386
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 324 CTGTCTCCAGAGCTGCTTTGAGGACTGCACTGACACTCCAGCGGCTCCAGAGGGGG 383
Oy 387 CCGCTGTGAGCAGTACAGCAGAGAGAAAGATATGATGATCAGCTTGTCTGACAGAG 446
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 384 CACTTCTAGAG---GACACAGGAGGAGACAGAAATGTGAATCATACCTTGTGAGACAG 440
Oy 447 ACCTCTCAGCATCAACAGACCGGCTGAGTTCACCT---CTCTGTAGAAATGGCCA 503
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 441 GCGCTCCACCATCAACAGACTGCTCTGATTTCCTCTCTGTATAGAACTGCTG 500
Oy 504 GTGCGATGAGAGTCCGGCAGACCGGCTCTGATTTCTTCTGCGAGTTCGCCCAATGCCA 563
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 501 GTGACAGGAGAGTCCAGAGCCAGCTCTCATTTCTTGTGAGCTCCCTTCCAAATACCA 560
Oy 564 CCCAGACCATGATATATAGAGTCTTGTGCTAGAACATATGACACACTCAGCTTGA 623
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 561 CTGTGAGCTTGAAGTGAAGTCTTGTGTGGTGGCTCAATATATACCACTCAGCTTGG 620
Oy 624 CAACTCAGTACGTGTGAGAGGTAATGCCAGTGGCTGAGTACCAAGCTTCTCTGGAGCTG 683
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 621 CTACTCAGTACGTGTGAGAGTGTGATGAGTGGCTGAGTGGCTCACTCCCTTGAAGGCTG 680
Oy 684 AACCTCAAGCTGTGTCAGCAGGAGACCTTACTGTGAGAGTGGTACCAAGAAACCCAGG 743
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 681 AACCTCAAGCTGTGTCAGCAGGAGGAGCTCAGCTGAGAGTGGTACTTGAAGGCTCAGG 740
Oy 744 TGGCCCAAGTCTCTGATCTTGGGCTGTGTTCCACAGGCTTTTGTGGCAGCCAGG 803
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 741 TACCCAGAGCTCAGTCTGCTGGTGGAGCTGCCATAGGCTTTTGTGGCAGCCCGG 800
Oy 804 TAAAGGTTGAGGCAAGCATCTCGGTTCCGGGAGAGTATGATTTGCCAGGAGGCTTCCA 863
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 801 TGAAGATTGGGGGCAAAACACCAAGATTCAACCGCAGAGCATGACAGAGAGGCTTCCA 860
Oy 864 GATATGCTGTGACAGCAAGATTTTGTAGACTTCCGTGAGATTTGGCTGAATGACTGGA 923
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 861 GATATGCTGTGACAGCAAGATTTTGTAGACTTCCGTGAGATTTGGCTGAGAGACTGGA 920
Oy 924 TCATCCAGCTGAAGGCTATGCAATGCAACTCTGACACTGGGCAATGCCACTATGATGG 983
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 921 TCATCCAGCTGAAGGCTATGCAATGCAACTCTGCAATAGGCGACTGCCACTACACTAG 980
Oy 984 CAGGATGCTGTGAGCTCTGCTCTCTTTCACACTGAGTGTGATCTGCTCAAGGCCA 1043
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 981 CAGGATGCTGTGAGCTCTGCTCTCTTTCACACTGAGTGTGATCTGCTCAAGGCCA 1040
Oy 1044 ACCGATGCTGTGAGCTCTGCTCTCTTTCACACTGAGTGTGATCTGCTCAAGGCCA 1103
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1041 ACACAGCTGTGAGGCAACCTGAGAGGCTCANNNTGTATACCAAGGCGCCGCGCCCG 1100
Oy 1104 TGTCTTGTCTACTATGACAGGAGCAAACTGTCAAGAGGAGATATGATGATGATG 1163
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1101 TGTCTTGTCTACTATGACAGGAGCAAACTGTCAAGAGTGTCAAGTGTGATGATGATG 1160

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Oy 1164 TGTGAGGAGGCTGTGGGTGTACTGATTTATGGTATACAGGCTGCTGAGTAGATG 1223
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1161 TGTGAGGAGGCTGTGGGTGTACTGATTTATGGTATACAGGCTGCTGAGTAGATG 1220
Oy 1224 G 1224
    |
Db 1221 G 1221

RESULT 5
ID AA047710 standard; cDNA to mRNA; 265 BP.
XX
XX AA047710;
AC
XX
XX
XX
XX 11-FEB-1994 (first entry)
DE
XX TGF-beta-like clone MP-121.
XX
XX Human; transforming growth factor; beta; TGF-beta; pharmaceutical;
KW bone; cartilage; tooth; wound repair; immunosuppressor;
KW organ transplant; cosmetic surgery; antibody; diagnosis; ss.
XX
XX Homo sapiens.
FH
FH Key Location/Qualifiers
FT CDS 2..265
FT /*lag- a
XX
XX MO9316099-A.
XX
XX 19-AUG-1993.
XX
XX 12-FEB-1993: 93WO-BP00350.
XX
XX 12-FEB-1992: 92EP-0102324.
XX
XX (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
XX
XX Hoelten G, Neidhardt H:
XX
XX WPI: 1993-272824/34.
XX
XX P-PSDB: AAR45447.
XX
XX
XX New transforming growth factor-beta family proteins and DNA
XX used in tissue and wound repair, in treatment of bone, cartilage
XX and tooth defects, and antibodies for diagnosis
XX
XX Claim 4: Page 18; 29pp: English.
XX
XX The sequences given in AA047709-10 represent embryo and liver derived
XX human transforming growth factor-beta (TGF-beta) genes respectively.
XX The proteins encoded by these sequences may be used in a pharmaceutical
XX composition for the treatment of various bone, cartilage or tooth
XX defects and in tissue and wound repair processes. These proteins
XX may also be used as immunosuppressors in organ transplants and in
XX cosmetic surgery. Antibodies raised against these proteins may be
XX used for diagnostic purposes.
XX
XX Sequence 265 BP: 58 A; 80 C; 69 G; 58 T; 0 other:

Query Match 13.6%: Score 212.2; DB 14; Length 265;
Best Local Similarity 87.5%; Pred. No. 4e-52;
Matches 232; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Oy 925 CATCAGCTGAAGGCTATGCAATGAACTTCTGACCTGGGCACTGCCACTAGTGTGGC 984
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 CATCAGCTGAAGGCTATGCAATGAACTTCTGCAATAGGAGAGTGGCCACTACACTAGC 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 985 AGGATGCTGTGAGCTCTGCTCTCTTTCACACTGAGTGTGATGATCTGCTCAAGGCCA 1044
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AGGATGCTGTGATTTCTCTCTCTTTCACACTGAGTGTGATGATCTGCTCAAGGCCA 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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YY 1045 CGCAGCTGCTGGCACACACTGGCAGAAGGGCTGTGTGTGCTCCATCAACATCTCGGCCCTT 1104
| | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 CACAGCTGCAGGCACCACTGAGGGGCTATGCTGTGTATCCACAGGCCCGGCCCTT 180
| | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1105 GTCTTGCTCTACTACTATACAGAGCAGCACAATTGTCAAGCGGANTATTCCTGACATGTT 1164
| | | | | | | | | | | | | | | | | | | | | | | | | |
DB 181 GTCTCTGTCTATATATAGCAGAGGAGCAGCATTTGCAAGACTGACATCTGACATGCT 240
| | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1165 GGTCCAGCCCTGCGCGTCTACTTAG 1189
| | | | | | | | | | | | | | | | | | | | | | | | | |
DB 241 AGTAGAGGCTGTGTGGTGCAGTTAG 265

RESULT 6
AAV38239
ID AAV38239 standard; DNA: 5099 BP.
XX AAV38239;
XX
XX
XX DT
XX
DE Nucleotide sequence of the genomic region between murine activin genes.
XX
KM Liver activin; beta c; beta e; cell differentiation; haematopoiesis;
KM erythroid; ovarian follicular maturation; hormone; neuronal survival;
KW spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;
KM osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunoassay;
menstrual disorder; transgenic; modulator; ss.
XX
XX Mus sp.
OS
PN WO9822492-A1.
XX
XX 28-MAY-1998.
PD
PF 20-NOV-1997; 97WO-US20882.
XX
PR 20-NOV-1996; 96US-0752919.
XX
PI (UNM1) UNIV MICHIGAN.
PA
PI Bonadio J, Fang J;
DR WPI; 1998-312408/27.
XX
PT New isolated nucleic acid encoding sub-units of liver activin -
PT useful for regulating growth and differentiation of cells, e.g. for
PT treating liver, bone and haematopoietic disorders
PS Disclosure; Fig 4B-C; 141pp; English.

This represents the nucleotide sequence of the genomic region between murine liver activin beta c and beta e genes. The invention relates to murine beta c and beta e polypeptides and the genes encoding them. Disorders of cell growth or differentiation (or susceptibility to them) are diagnosed by measuring liver activin gene activity or by detecting a mutation in the liver activin gene. Disorders of haematopoiesis, erythroid differentiation, ovarian follicular maturation, hormone secretion, neuronal survival, spermatogenesis, bone formation, insulin secretion, or cardiac morphogenesis are some conditions that can be stimulated using the liver activin. Cell growth and differentiation can be stimulated by treatment with an liver activin compound or agent that upregulates the compound's expression. Antagonists can be used to treat liver diseases while agonists can be used to increase growth and regeneration of liver tissue. The liver activin compound may also induce bone growth (e.g. for treating osteoporosis or osteomalacia) or haematopoiesis, particularly erythropoiesis, e.g. for treating hemophilia, cystic fibrosis or menstrual disorders. Antibodies are useful in immunoassays, to generate anti-idiotypic antibodies (which bind to liver activin receptors) and to inhibit liver activin. Also, transgenic animals containing liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins,

CC	or the transgenic animals, are useful for screening for liver activin modulators.
XX	
XX	
So	Sequence 5099 BP; 1305 A; 1425 C; 1154 G; 1215 T; 0 other:
	Query Match 10.9%; Score 169.2; DB 19; Length 5099;
	Best Local Similarity 88.0%; Pred. No. 7,2e-39;
	Matches 220; Conservative 0; Mismatches 23; Indels 7; Gaps 3
OY	1315 GGATCACCCTCTTAAAGAGCTCACTAGTACCAACACCCCTTCTCTCTCTCCGAGACATGG 1374
Db	1 GGATCACCCTCTTAAAGAGCTCACTAGTACCAACACCCCTTCTCTCTCTCCGAGACATGG 60
OY	1375 TTGACCCAGTACACCCATCTCTGACGCTTAAAGTAAAGGGCTATGACTCTACATATA-- 1432
Db	61 TTGACCCAGTACACCCATCTCTGACGCTTAAAGTAAAGGGCTATGACTCTACATATA-- 120
OY	1433 -TATGTCATTTTGTCTCTA--CAACACCCCTTAACTCCCTTGTGTACATATGTAATC 1488
Db	121 CAATGTCAATTTGTCTCTGCAACACACCCCTTAACTCCCTTGTGTACATATGTAATC 180
OY	1489 TACTCTGCTCCCTCCGACCCGCGACCGGAGGTTCCTATTCACATGATATGCTTAGT 1548
Db	181 TACTCTGCTCCCTCCGACCCGCGACCGGAGGTTCCTATTCACATGATATGCTTAGT 239
OY	1549 GTCTCCCTT 1558
Db	240 GTCTCCCTT 249
RESULT 7	
AAV38238	
ID	AAV38238 standard; cDNA: 2125 BP.
XX	
AC	AAV38238;
XX	
DT	01-FEB-1999 (first entry)
XX	
DE	Murine liver activin beta e polypeptide encoding cDNA.
XX	
KW	liver activin; beta c; beta e; cell differentiation; haematopoiesis;
KW	erythroid; ovarian follicular maturation; hormone; neonatal survival;
KW	spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;
KW	osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunosassay;
KW	menstrual disorder; transgenic; modulator; ss.
XX	
OS	Mus sp.
XX	
FH	Key Location/Qualifiers
FT	CDS 216..1268
FT	/*tag= a
FT	/product= "activin beta e polypeptide"
FT	sig_peptide 216..278
FT	/*tag= b
FT	mat_peptide 279..1265
FT	/*tag= c
XX	
PN	W09822492-A1.
XX	
PD	28-MAY-1998.
XX	
PF	20-NOV-1997; 97MO-US20882.
XX	
PR	20-NOV-1996; 96US-0752919.
XX	
PA	(UNMI) UNIV MICHIGAN.
PI	Bonadio J, Fang J;
XX	
DR	WPI; 1998-312408/27.
XX	
DR	P-PSDB; AAM60618.
XX	
PT	New isolated nucleic acid encoding sub-units of liver activin -

XX	Fertility control; contraception; hormone; spermatogenesis; ss.
OS	Homo sapiens.
XX	
XX	
FT	Key Location/Qualifiers
FT	CDS 3..716
FT	/*tag= a
FT	mat_peptide /product=hydrophobic signal sequence a pro-region
FT	717..1061
FT	/*tag= b
XX	
PX	EP222491-A.
PN	
PD	20-MAY-1987.
XX	
PF	02-OCT-1986; 86EP-0307586.
XX	
PR	12-SEP-1986; 86US-0906729.
PR	03-OCT-1985; 85US-0783910.
PR	10-FEB-1986; 86US-0827710.
PA	(GETH) GENENTECH INC.
PI	Mason AJ, Seeburg PH;
DR	WPI: 1987-137512/20.
DR	P-PDB: AAP70204.
XX	
PT	Recombinant human or porcine inhibin or activin - used for
PT	modulating clinical condition or reproductive physiology of
PT	animals.
PS	Disclosure; Fig 9A; 48pp; English.
XX	
CC	A compsn. comprising human or porcine inhibin which is completely
CC	free of unidentified or porcine proteins is claimed. Also claimed
CC	are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta
CC	chain. Sequencing of inhibin-encoding cDNA has led to the
CC	identification of prodomain regions located N-terminal to the
CC	mature inhibin chains that represent coordinately expressed
CC	biologically active polypeptides. The prodomain regions or
CC	prodomain immunogens are useful in monitoring preproinhibin
CC	processing in transformant cell culture or in experiments directed
CC	at modulating the climical cond. or reproductive physiology of
CC	animals.
SQ	Sequence 1966 BP; 424 A; 557 C; 621 G; 364 T; 0 other:
Query Match	8.3%; Score 129.4; DB 8; Length 1966;
Best local Similarity	58.9%; Pred. No. 2..2e+27;
Matches 261; Conservative	0; Mismatches 176; Indels 6; Gaps
OY	743 GTGGCCACAGATTCTTGATCCTGGGCTGTTCGCCACAGAAGCGTTTGTGGCACGCCAG 802
Db	618 GTGGTCCCGGTTGTCGTGCACCAGCGGAAGACTGCACCGGCGCTTTGTGTGTCAG 677
OY	803 GTAAG---GGTTAGGGGACAGATCGGATTGCGCGGCGAGATATCATTTGCCAGAGGGGG 859
Db	678 GCTCGGCTGGCGCAGACAGACGCCATTCGCAAGCGAGCGCTGGAGTGCATGGCCGG 737
OY	860 TCAGAGATGTGCTGTGCACAAGACTTTTTTGTAGACTTCCGTGAGATTGGCTGGAATGAC 919
Db	738 ACCAACTCTGTGGCAGGCAACACTTCTTATGTAGACTTCGCGCTCATGGCTGGAACGAC 797
OY	920 TGCAATATCCAAGCTGANAAGCTATGCCATGAAGCTTCGCACTGGAGCGGAGTCCCACATACAT 979
Db	798 TGGATCATTAACACACCACCGGCTACTACGGGAATCTAGTAGAGGAGAGACTGCCACGCTAC 857
OY	980 GTGACAGGCAATGCCTGGACCTCTTGCCCTTTCCATCACTSCAGATGCTGAATCTGCTCAA 1039
Db	858 CTGGCAGAGGGGCCCCGGGCTGCTCTCTTCACACAGGCGTGGTGGAACAG--TAC 914
OY	1040 GCCAACGACAGTCTGTGCACCACTGTGGAGAGGGGCTGTGTGCGTGCGCTACATCTCGGCGC 1099

```

Db      915 CGCATGGGGGTCGTGAACCCCGGCAGCGTGAACCTCCGCTGATTCGCCAACCAAGCTGAGC   974
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      1100 CCTGTGCTTTGTTCTCTACTATGACAGGACAGACAATTTCAGAAGCGATATACCTGAC   1159
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      975 ACCATGTCATGCTGTACTTCGATGATGAGTACGACACACATCTCTCAAGGAGCGTGCCCAAC   1034
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Cy      1160 ATGTTGTCGAGCGGCTGCGGGTG   1182
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      1035 ATGATTGTGAGAGTGGGCTG   1057

RESULT 13
AAN70318
ID      AAN70318 standard; cDNA; 1530 BP.
XX
XX      AAN70318:
XX
XX      09-APR-1991 (first entry)
XX
DE      Sequence encoding porcine inhibin beta-chain precursor beta-B.
XX
KM      Fertility control; contraception; hormone; spermatogenesis; ss.
XX
OS      Sus scrofa domestica.
XX
Key      Location/Qualifiers
FH      CDS               1..810
FT              /*tag= a
FT              /product=hydrophobic signal sequence a pro-region
FT              811..1160
FT              /*tag= b
XX
XX      mat_peptide
XX
XX      EP222491-A.
XX
PD      20-MAY-1987.
XX
XX      PF      02-OCT-1986;    86EP-0307586.
XX
XX      PR      12-SEP-1986;    86US-0906729.
XX      PR      03-OCT-1985;    85US-0783910.
XX      PR      10-FEB-1986;    86US-0827710.
XX
PA      (GENE ) GENENTECH INC.
XX
XX      PI      Mason AJ, Seeburg PH;
XX
DR      WPI: 1987-137512/20.
XX      DR      P-PSTDB: AAP70201.
XX
PT      Recombinant human or porcine inhibin or activin - used for
PT      modulating clinical condition or reproductive physiology of
PT      animals.
XX
PS      Disclosure; Fig 1B; 48pp; English.
XX
XX
CC      A compsn. completing human or porcine inhibin which is completely
CC      free of unidentified or porcine proteins is claimed. Also claimed
CC      are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta
CC      chain. Sequencing of inhibin-encoding cDNA has led to the
CC      identification of prodomain regions located N-terminal to the
CC      mature inhibin chains that represent coordinately expressed
CC      biologically active polypeptides. The prodomain regions or
CC      prodomain immunogens are useful in monitoring preproinhibin
CC      processing in transformant cell culture or in experiments directed
CC      at modulating the clinical condn. or reproductive physiology of
CC      animals.
XX
XX      Sequence 1530 BP; 318 A; 469 C; 511 G; 232 T; 0 other;
SQ
Query Match          7.8%; Score 121; DB 8; Length 1530;
Best Local Similarity 56.2%; Pred. No. 5,7e-25;
Matches 251; Conservative 0; Mismatches 190; Indels 6; Gaps

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OY 743 GTGGCCACAGTTCCTGATCCCTGGGCTGTTTCCACAGGCGCTTTTGGCCAGCCAG 802
 DB 604 GTGGTCCCGGCTGTTTGTGAGCCGCGGCGACAGTACACCGGCTTGTGGTGTGAG 663
 OY 803 GTTAAAGGCTTGAAGGCA-----AGCATCGGGTCCCGGCGAGGTATGATGGCAGGG 856
 DB 664 GCGCCACATGGGTGACAGAGAGGCGCCCGCATCCGCAAGCGGCGCTGAGTGTGAGGGC 723
 OY 857 GGGTCAGGATGCTGCTGACAGAGATTTTGTAGACTTCCTGAGATTGGCTGGAAT 916
 DB 724 CGGACCAACCTCTCTTGGACGACAGTCTTTCATTCACATTCGCCCTCATTTGGCTGAGT 783
 OY 917 GACTGGATCATCAGCTGAAAGCTTATGCCATGAACTTGTGACTGGCAGTCCGCACTA 976
 DB 784 GACTGATCATCAGCGCCACCGCGCTACTATGGAAGTACTGTAGGGCAGCTGTCCGGCC 843
 OY 977 CATGTGGAGGAGGATCGGCGGATCTGCTCCCTTTCACACTGAGTGTGAATGTGCTC 1036
 DB 844 TACCTGGAGAGGGGTGCGAGGCTCCGCTCATCTTCCACAGCGCGGTGTCACAGTAC 903
 OY 1037 AAAGCCAAAGCAGCTGCTGCGACCATGCGAGGGGCTGCTGCGCTTACATCTCGG 1096
 DB 904 CGCATGCGGCGGCTGACACCGGCTGCGGACAGTGAACCTCTGCTGATCCCGCAAGCTG 963
 OY 1097 CGCCCTCTCTCTTGTCTCTACTATGACAGGAGACACATTTGTCAAGACGATATACCT 1156
 DB 964 AGCAGCATGTCTCATGCTCTACTTGTGATGAGAGAGTACAACTCTCAAGCGGGGACGTGCC 1023
 OY 1157 GACATGTGTGTGAGGCTCGCGGTGT 1183
 DB 1024 AACATGATCGTGAAGAGTGTGGCTGT 1050

RESULT 14

AAN70317
 ID AAN70317 standard; cDNA: 3588 BP.

AC AAN70317;
 DT 09-APR-1991 (first entry)
 DE Sequence encoding porcine Inhibin beta-chain precursor beta-A.
 XX Fertility control; contraception; hormone; spermatogenesis; ss.
 OS Sus scrofa domestica.
 XX
 FH Key Location/Qualifiers
 FT CDS 34..957
 FT /tag= a
 FT /product=hydrophobic signal sequence a pro-region
 FT 958..1307
 FT /tag= b
 FT 3551..3556
 FT /tag= c
 XX
 PN EP222491-A.
 PD 20-MAY-1987.
 PF 02-OCT-1986; 86EP-0307586.
 PR 12-SEP-1986; 86US-0906729.
 PR 03-OCT-1985; 85US-0783910.
 PR 10-FEB-1986; 86US-0827710.
 XX (GETH) GENENTECH INC.
 PA Mason AJ, Seeburg PH;
 PI
 DR WPI: 1987-137512/20.
 FR P-PsDB: AAP70200.

XX Recombinant human or porcine inhibin or activin - used for
 PT modulating clinical condition or reproductive physiology of
 PT animals.
 XX
 PS Disclosure: Fig 1B; 48pp; English.

CC A compen. comprising human or porcine inhibin which is completely
 CC free of unidentified or porcine proteins is claimed. Also claimed
 CC are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta
 CC chain. Sequencing of inhibin-encoding cDNA has led to the
 CC identification of prodomain regions located N-terminal to the
 CC mature inhibin chains that represent coordinately expressed
 CC biologically active polypeptides. The prodomain regions or
 CC prodomain immunogens are useful in monitoring preproinhibin
 CC processing in transformant cell culture or in experiments directed
 CC at modulating the clinical cond. or reproductive physiology of
 CC animals.

SO Sequence 3588 BP; 881 A; 986 C; 998 G; 723 T; 0 other;

Query Match 7.7%; Score 120.4; DB 8; Length 3588;
 Best Local Similarity 57.4%; Pred. No. 1.3e-24;
 Matches 217; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

OY 812 GAGGCAAGCATCGGCTTCCCGCGAGTATGATTCGACAGGGGGGTCCAGATGTGC 871
 DB 931 GAGCAACCCCGACCGCCCGCGGCGGCTGAGTGGACGCGCAAGGTCAACATCTGC 990
 OY 872 TGTGCAAGAGTATTTTGTAGACTTCCGAGATTTGGCTGGAATGACTGATCATCCAG 931
 DB 991 TGTAAAGCAGCTTCTTGTACATTTCAAGACATGCGCTGGAACGACTGATCTCCCT 1050
 OY 932 CTTGAAGCTATGCAATGAATCTTGCACATGGGAGTGGCCCACTAATGTGGCGCATG 991
 DB 1051 CCGTCCGGCTTACACGCAACTACTCGAGGGCGAGTCCCGCAGCAATATAGCGGCGACG 1110
 OY 992 CTTGGATCTCTGCTCTCTTTCACACTGCGAGTGTGATCTCTCAAGGCCAAGCCACT 1091
 DB 1111 TCGGGGCTCTGCTCTCTGTTCCACTGAGGCTATCAACCACTACGATGGCGGCCAC 1170
 OY 1052 GCTGGACACACTGGCAGAGGGCTGCTGCTGCTGCTTACATCTGGGCGCCCTGCTTTG 1111
 DB 1171 AGCCCTTTCGCCAACCCTCAAGTCTGCTGCTGCCACCAACCTGAGGCCATGTCCATG 1230
 OY 1112 CTCTACTATGACAGGAGACAGCAACATTTGCAAGCGGATATACATGATGTGTGAG 1171
 DB 1231 CTGTACTACGACGCGGCGAGAACATCATCAAGAGACATCCAGAACATGATCTGGAG 1290
 OY 1172 GCCTGCGGGGTGTAGTTAG 1189
 DB 1291 GAGTGGCGGGTGTCTCTAG 1308

RESULT 15

AAH57530
 ID AAH57530 standard; cDNA: 1620 BP.

AC AAH57530;
 DT 10-SEP-2001 (first entry)
 DE Human pancreas cell specific cDNA sequence SEQ ID NO:370.
 XX
 KW Human; tissue specific; diagnosis; brain; heart; skeletal muscle;
 KW lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;
 KW metabolic disease; developmental disease; cytostatic; immunomodulatory;
 KW neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
 XX
 OS Homo sapiens.
 PN WO200132927-A2.

PD 10-MAY-2001.

XX 02-NOV-2000; 2000WO-US30396.

XX 04-NOV-1999; 99US-0163508.

XX (INCY-) INCYTE GENOMICS INC.

XX Sornasse T, Sellhamer JJ, Watson GA;

XX WPI: 2001-291057/30.

XX New cell and tissue specific polynucleotides useful for diagnosis,
XX prognosis or monitoring of treatments for disorders where the gene is
XX associated with a cancer, immunopathology or neuropathology -

PS Claim 1: Page 287-288; 327pp: English.

XX AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
XX sequences (I). (I) can have cytosstatic, immunomodulatory and
XX neuroprotective activities, and can be used in gene therapy. (I) and
XX proteins (II) encoded by then are used in high throughput screening
XX assays to select DNA molecules, RNA molecules, peptide nucleic acids,
XX mimetics, peptides, proteins, agonists, antagonists, antibodies or
XX their fragments, immunoglobulins, inhibitors, drug compounds and
XX pharmaceutical agents. Expression of (I) in a sample indicates the
XX differentiation of embryonic stem cells into a tissue selected from
XX brain, heart, kidney, liver, lung, skeletal muscle or pancreatic
XX tissues. (I) and (II) are used to produce an expression profile that
XX defines a metabolic or developmental process, treatment, condition,
XX disease or disorder. The gene profile can be used for diagnosis,
XX prognosis or monitoring of treatments and for investigating a
XX predisposition to a disorder where the gene is associated with a
XX cancer, immunopathology or neuropathology.

SQ Sequence 1620 BP; 475 A; 377 C; 476 G; 291 T; 1 other;

Query Match 7.5%; Score 116.4; DB 22; Length 1620;

Best Local Similarity 55.8%; Pred No. 1.3e-23;

Matches 222; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

OY 792 TGGCAGCCCGAGTAAAGGTTGAGGCGCAAGCATGGGTTGCGCGGAGGTATGATGCC 851
DB 1099 TGCAGAGCCCGGCACTGTGAGACACCCCTCATCGCGGCGCTTGGAATGTG 1158
OY 852 AGGGGGGTCCAGATGTGCTGTCGACAAAGATTTTGTAGACTCCGTGAGATGGCT 911
DB 1159 ATGGCAAGCTCAACATCTGCTGTAAGAAAGTTCTTGTCACTTCAAGACATCGGCT 1218
OY 912 GGAATGACTGATCATCCAGCTGAAGCTATGCAATCTTGCACATGCGGAGTGGC 971
DB 1219 GGAATGACTGATCATCTGCTCTGCTATCATGCCAATCTACTGCGAGGTGATGCC 1278
OY 972 CACTACATGTGCGAGCATGCGCTGTCCTGCTTCACTGCACTGCACTGCAATC 1031
DB 1279 CGAGCATATAGCAGCAGCTCCGGCTCTCATCTCTTCACATCAACAGTCAACCC 1038
OY 1032 TGCTCAAGCCCAAGCAGCTCTGCGACACCTGCGAGGGGCTGCTGCTGCTACAT 1091
DB 1339 ACTACCGGATCGGGGCGCATAGCCCTTTGCAACCTCAATCTGCTGTGCGCCACCA 1398
OY 1092 CTCGCGCCCTCTCTCTTGTCTTACTATGACAGGACAGCAATGTCAGAGGATA 1151
DB 1399 AGCTAGAGCCCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1458
OY 1152 TACCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1189
DB 1459 TTCAGAACATGATCGTGGAGAGAGTGTGGTGTGCTCATAG 1496

2000

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2002, 16:51:16 ; Search time 36.2042 Seconds
(without alignments)
10570.520 Million cell updates/sec

Title: US-09-684-383-3

Perfect score: 1558
Sequence: 1 AAGGAGTCATGCCACTCGCA.....ATGCCTTAGTCTCTCCCTT 1558

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
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5: /cgn2_6/ptodata/1/lna/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1558	100.0	1558	1	US-08-482-577B-3	Sequence 3, Appl
2	1558	100.0	1558	4	US-09-218-176-3	Sequence 3, Appl
3	781	50.1	2272	1	US-08-482-577B-1	Sequence 1, Appl
4	781	50.1	2272	4	US-08-289-222E-2	Sequence 2, Appl
5	781	50.1	2272	4	US-09-218-176-1	Sequence 1, Appl
6	781	50.1	2272	4	US-09-054-526B-2	Sequence 2, Appl
7	212.2	13.6	265	4	US-08-289-222E-5	Sequence 5, Appl
8	212.2	13.6	265	4	US-09-054-526B-5	Sequence 5, Appl
9	143.4	9.2	687	1	US-08-455-550-2	Sequence 2, Appl
10	137	8.8	2419	2	US-08-765-662-13	Sequence 13, Appl
11	137	8.8	2419	5	PCT-US95-08745-13	Sequence 13, Appl
12	136	8.7	360	2	US-08-274-215A-11	Sequence 11, Appl
13	136	8.7	360	2	US-08-765-662-11	Sequence 11, Appl
14	136	8.7	360	2	US-09-184-833-11	Sequence 11, Appl
15	136	8.7	360	5	PCT-US95-08745-11	Sequence 11, Appl
16	129.4	8.3	1966	1	US-08-197-792-44	Sequence 44, Appl
17	129.4	8.3	1966	1	US-08-459-850-44	Sequence 44, Appl
18	129.4	8.3	1966	1	US-08-459-850-44	Sequence 44, Appl
19	127	8.2	1524	1	US-08-197-792-34	Sequence 34, Appl
20	127	8.2	1524	1	US-08-459-850-34	Sequence 34, Appl
21	127	8.2	1524	1	US-08-459-850-34	Sequence 34, Appl
22	120.4	7.7	3588	1	US-08-197-792-32	Sequence 32, Appl
23	120.4	7.7	3588	1	US-08-459-850-32	Sequence 32, Appl
24	120.4	7.7	3588	1	US-08-459-850-32	Sequence 32, Appl
25	116.4	7.5	1633	1	US-08-197-792-42	Sequence 42, Appl
26	116.4	7.5	1633	1	US-08-459-850-42	Sequence 42, Appl
27	116.4	7.5	1633	1	US-08-459-214-42	Sequence 42, Appl

28	93.4	6.0	1667	1	US-08-455-550-1	Sequence 1, Appl
29	70.4	4.5	926	1	US-08-362-670B-1	Sequence 1, Appl
30	70.4	4.5	926	3	US-08-333-576C-1	Sequence 1, Appl
31	70.4	4.5	926	4	US-08-808-324-1	Sequence 1, Appl
32	70.4	4.5	926	5	PCT-US94-14030A-1	Sequence 3, Appl
33	70.4	4.5	1345	3	US-08-362-670B-33	Sequence 33, Appl
34	70.4	4.5	1345	3	US-08-333-576C-33	Sequence 33, Appl
35	70.4	4.5	1345	3	US-08-808-324-33	Sequence 33, Appl
36	70.4	4.5	1345	5	PCT-US94-14030A-33	Sequence 33, Appl
37	68.2	4.4	420	1	US-08-360-914B-11	Sequence 11, Appl
38	68.2	4.4	420	1	US-08-741-589A-11	Sequence 11, Appl
39	68.2	4.4	420	5	PCT-US94-13181-11	Sequence 11, Appl
40	68.2	4.4	1003	1	US-07-800-364B-13	Sequence 13, Appl
41	68.2	4.4	1003	2	US-07-989-847-11	Sequence 11, Appl
42	68.2	4.4	1003	4	US-08-469-411-11	Sequence 11, Appl
43	68.2	4.4	1723	1	US-07-841-646-28	Sequence 28, Appl
44	68.2	4.4	1723	1	US-07-901-703-10	Sequence 10, Appl
45	68.2	4.4	1723	1	US-08-147-023-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-482-577B-3
Sequence 3, Application US/08482577B
Patent No. 5807713
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKALDO, MARIELSTEIN, MURRAY, AND ORAM
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,577B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, SHARON
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P564-5010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1558 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PUBLICATION INFORMATION:
DOCUMENT NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
US-08-482-577B-3
Query Match 100.0% Score 1558; DB 1; Length 1558;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

OY	1081	CGGGCTTCACATCTGGGGGCCCTCTGCTCTTGGCTCTACTATGACAGGGACACCAACTTGT	1140
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Db	1141	CAAGACGGATATACCTGACATGTGTGTGTCAGAGGCTCCGGGTATGTTAGCTTATGGTGA	1200
OY	1201	TACAGGGCTCGCTGAGGTATGAATGGCCCTTCTCAGGAGGAAACTCTGTTCCCACTTCTG	1260
Db	1201	TACAGGGCTCGCTGAGGTATGAATGGCCCTTCTCAGGAGGAAACTCTGTTCCCACTTCTG	1260
OY	1261	TCGAGAAATGGAACACCTTCTTAAGCATGACAGATCCCTCTGTGTGACTTCAGGGGATCC	1320
Db	1261	TCGAGAAATGGAACACCTTCTTAAGCATGACAGATCCCTCTGTGTGACTTCAGGGGATCC	1320
OY	1321	ACCTCTTAAGAGAGTCACTAGTACCAACAGCCCTTCTCTCTCGTGGAGCATGGTTGACC	1380
Db	1321	ACCTCTTAAGAGAGTCACTAGTACCAACAGCCCTTCTCTCTCGTGGAGCATGGTTGACC	1380
OY	1381	CAGTACACCCATCCTCGACCTTAAGTTAGAGGGCTAATGACATCCATATATATATGAT	1440
Db	1381	CAGTACACCCATCCTCGACCTTAAGTTAGAGGGCTAATGACATCCATATATATATGAT	1440
OY	1441	TTTGTCTCTAGCAAAACACCCCTTAGCTCCCTTAGTCAACATATATATCTACTCGCTCC	1500
Db	1441	TTTGTCTCTAGCAAAACACCCCTTAGCTCCCTTAGTCAACATATATATCTACTCGCTCC	1500
OY	1501	CTGACCCCTGGCACCGGAAGTTCCTATTCACAGATGATATGCTTAGTGTCTCCCTTT	1558
Db	1501	CTGACCCCTGGCACCGGAAGTTCCTATTCACAGATGATATGCTTAGTGTCTCCCTTT	1558

US-09-218-176-3
Sequence 3, Application US/09218176
Patent No. 6171584
GENERAL INFORMATION:
APPLICANT: H TITEN, Gertrud
APPLICANT: NEIDHARDT, Helge
APPLICANT: BECHTOLD, Rolf
APPLICANT: POHL, Jens
APPLICANT: PAULISTA, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
TITLE OF INVENTION: TGF- FAMILY
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIKAIIDO, MARNELESTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., G Street Lobby,
STREET: Suite 330
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218,176
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,048
FILING DATE: 12-JUL-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03065
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA: PCT/EP93/00350

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: FILING DATE: 2-FEB-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/482,577
: FILING DATE: 7-JUN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: EP 92 102 324.8
: FILING DATE: 12-FEB-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE P 44 23 190.3
: FILING DATE: 01-JUL-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 195 11 243.1
: FILING DATE: 27-MAR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: KITS, Monica Chln
: REGISTRATION NUMBER: 36,105
: REFERENCE/DOCKET NUMBER: P5610-6010
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202/638-4810
: TELEFAX: 202/638-5000
: INFORMATION FOR SEQ. ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1558 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
US-09-218-176-3

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Query Match      100.0%; Score 1558; DB 4; Length 1558;
Best local similarity 100.0%; Pred. No. 0;
Matches 1558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AAGGAGCATGCGGAGGTGAGTCAATCCCTCCAGGTCCTGGTGGCCAGGAC 60
DB 1 AAGGAGCATGCGGAGGTGAGTCAATCCCTCCAGGTCCTGGTGGCCAGGAC 60
QY 61 AGAGTTGAACACTCCGTTGAGACCTGAAATAGCTTTGGGCTTTAAGAGGCTA 120
DB 61 AGAGTTGAACACTCCGTTGAGACCTGAAATAGCTTTGGGCTTTAAGAGGCTA 120
QY 121 TCTCCAGCAATGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
DB 121 TCTCCAGCAATGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
QY 181 AGTGAACCCCAAACTAGAGGTCCATGCCAGATGTTGGGGTCCATCTTGAAC 240
DB 181 AGTGAACCCCAAACTAGAGGTCCATGCCAGATGTTGGGGTCCATCTTGAAC 240
QY 241 GAGCAGCGGAGGAGCTGCTTCGATTTGGCCAGAAAGTATCTGAGCAAGCTG 300
DB 241 GAGCAGCGGAGGAGCTGCTTCGATTTGGCCAGAAAGTATCTGAGCAAGCTG 300
QY 301 CAGCAGCGGCGCCATCTAGTGGGCGAGTGTCCAGAGGGGCTCTCAAGAC 360
DB 301 CAGCAGCGGCGCCATCTAGTGGGCGAGTGTCCAGAGGGGCTCTCAAGAC 360
QY 361 GCGGCTCGGGGGGCTGAGGGGAAACCTGTTGAGCATGAGCAGAGCAAGATA 420
DB 361 GCGGCTCGGGGGGCTGAGGGGAAACCTGTTGAGCATGAGCAGAGCAAGATA 420
QY 421 TGAGATCAGCTTTGCTGACAGACACTCTCCAGCATCAACGAGCCGCTGAG 480
DB 421 TGAGATCAGCTTTGCTGACAGACACTCTCCAGCATCAACGAGCCGCTGAG 480
QY 481 CCACCTTCTGTGTAATGGCAGCTGAGAGTCCGCGAGACCCGCTTCAATG 540
DB 481 CCACCTTCTGTGTAATGGCAGCTGAGAGTCCGCGAGACCCGCTTCAATG 540
QY 541 CGTGCAGTCCCGCAATGCGACCCAGACCATGAAATATAGATTCTTGTGTA 600
DB 541 CGTGCAGTCCCGCAATGCGACCCAGACCATGAAATATAGATTCTTGTGTA 600

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QY 601 AATGACACCAACTCTACCTTGACAGTCACTAGTGTGAGGTGAATGCCAGTG 660
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QY 661 GTACCAAGCTTCTCTGAGCACTGAAAGCTCAAGCTCTGAGCCAGGACACTT 720
DB 661 GTACCAAGCTTCTCTGAGCACTGAAAGCTCAAGCTCTGAGCCAGGACACTT 720
QY 721 GGAGCTGTGACAGAAAGCCAGTGGCCACAGTTCCTGATCCCTGGGCTTTT 780
DB 721 GGAGCTGTGACAGAAAGCCAGTGGCCACAGTTCCTGATCCCTGGGCTTTT 780
QY 781 CAGGCTTTTGTGCGACCCAGCAAGTAAAGGTGAGGCAAGCATTCGGTTCG 840
DB 781 CAGGCTTTTGTGCGACCCAGCAAGTAAAGGTGAGGCAAGCATTCGGTTCG 840
QY 841 TATCGATTCCAGGGGGGCTCCAGCATGCTGTGACAAAGTTTTTTGTGACT 900
DB 841 TATCGATTCCAGGGGGGCTCCAGCATGCTGTGACAAAGTTTTTTGTGACT 900
QY 901 TGAGATTGCTGGAATGACTGGATCCAGCCTGAAGCTATGCGATGAATCTG 960
DB 901 TGAGATTGCTGGAATGACTGGATCCAGCCTGAAGCTATGCGATGAATCTG 960
QY 961 TGGGAGTCCCGCACTACATGTGGCAGGCAATGCTGCGCATCTCTGCTTCA 1020
DB 961 TGGGAGTCCCGCACTACATGTGGCAGGCAATGCTGCGCATCTCTGCTTCA 1020
QY 1021 AGTGTGAATCTGTCTTAAAGCCAGCAGCTGTGACACACTGGCAGGGGCT 1080
DB 1021 AGTGTGAATCTGTCTTAAAGCCAGCAGCTGTGACACACTGGCAGGGGCT 1080
QY 1081 CGGCTTACATCTCGGCGGCTCTGTCTTGTCTGCTATGCTAGAGGAGCA 1140
DB 1081 CGGCTTACATCTCGGCGGCTCTGTCTTGTCTGCTATGCTAGAGGAGCA 1140
QY 1141 CAAGAGGATATACCTGACATGGTGTGAGGCTGCGGGGTAGTTAGCTTA 1200
DB 1141 CAAGAGGATATACCTGACATGGTGTGAGGCTGCGGGGTAGTTAGCTTA 1200
QY 1201 TACAGCTGCTGAGTAAATGCGCTTCTGAGGAAAGGAAATCTGTTCC 1260
DB 1201 TACAGCTGCTGAGTAAATGCGCTTCTGAGGAAAGGAAATCTGTTCC 1260
QY 1261 TCCAGATGAAGAAACCTTTCTAAGCATGACATCCCTGTGAGCTTCA 1320
DB 1261 TCCAGATGAAGAAACCTTTCTAAGCATGACATCCCTGTGAGCTTCA 1320
QY 1321 ACCCTTAAAGAGTCACTAGTACCAACAGCCTTCTCTCTGAGCATG 1380
DB 1321 ACCCTTAAAGAGTCACTAGTACCAACAGCCTTCTCTCTGAGCATG 1380
QY 1381 CAGTACACCATCTCTAGCTTAAGTTAGAGGTAAATGCAATATATATAT 1440
DB 1381 CAGTACACCATCTCTAGCTTAAGTTAGAGGTAAATGCAATATATATAT 1440
QY 1441 TTTGCTCTGAGCAAAACCCCTTATGCTCCCTTATGATATATATATAT 1500
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QY 1501 CTGACCTCGCACCGAAGGTTCTATTCACAGATATATGCTTATGCTT 1558
DB 1501 CTGACCTCGCACCGAAGGTTCTATTCACAGATATATGCTTATGCTT 1558

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RESULT 3
US-08-482-577B-1
: Sequence 1, Application US/08482577B
: Patent No. 5807713
: GENERAL INFORMATION:
: APPLICANT: HOTTEN, GERTRUD
: APPLICANT: NEIDHARDT, HELGE
: APPLICANT: BECHTOLD, KOLF

```


Query Match	50.1%	Score 781	DB 4	Length 2272
Best Local Similarity	79.9%	Pred. No. 3,4e-229		
Matches	959	Conservative	0	Mismatches 235; Indels 7; Gaps
QY	28	CACATTCCTCCACAGGCTGCCCTGGTCCCGCAGACAGAGATTGA-AGCACTCCCTGGAGACC	86	
Db	24	CACACTTCCTCCAGGGCTCTCGGACGCCAGAGATTAGACACACACTTTTAGACC	83	
QY	87	CTGAATTTAGGCTTTTGGGTCTTTTAAAGAGGCTTATCTCCAGCAATGGGCTTCCTTGGC	146	
Db	84	CTGAGCCCTGAGCTGTGTATTATTTGGTCAAGAGAGGGCCCTTCCAGCAATGAGACTCTCATTTGC	145	
QY	147	TCCGAGCTCTTGTTGTTCCCTGACTCCCAACACACAGTAGTGAACCCCAAACTGAGGTCAT	205	
Db	144	TTTCGGGCTTTCTCTCTCTCGGCTCCACACACAGTGGCACTCCCAAGTGGGGCTGACT	203	
QY	207	GCCGAGCATGTTGGGGTGGCATCTTTGACCTGAGAGACCAGCGGAGCTGTCTGCATT	266	
Db	204	GTCGACATGTGGGGGGGCCCACTTGGAACTGGAGAGACCAGGGGAGAGCTCTTTGATTC	265	
QY	267	TGGCCAGAAAGAAAGTATCTCTGGACAAGCTGCACCTCAGGCCAGCGCCCATACTAGTCGGC	326	
Db	264	TGGCCAAAGAAAGCACTTTGGCAAGCTGCACCTCAGGCCAGCGCCCAACACTGAAGCGCC	322	
QY	327	CAGTGTCCAGAGGGGGCTCCAAAGACCGCGCTGCAGCGCCCTCCCGCGGGCTGCAGCGGAA	386	

Db	324	CTGTGTCCAGAGTGTGTTTGAGAGTGTGCACACTGTCCAGAGGGATGCCACAGAGGG	383
Qy	387	CCGTGTTTGGAGATGACCAGAGCAAGAAATATGATATATACGTTTCTGTACACAG	446
Db	384	CATTTCCTAAG---GACACAGAGGAAACAGAAATGTGAATATATAGCTTTGTGACAG	440
Qy	447	ACCTTCCAGATCAACAGACCCCGGCTCGAGTTCACCT---CTGTGTAGAATGGCCA	503
Db	441	GCCCTCCACACTCAACCCAGACTCTGTTGATTTTTCACCTTCTCCTGTGATAGAACTGCTG	500
Qy	504	GTGGCATGGAGATCCCGCAGACACCCTTCATGTTCTTGTGTGCAATTTCCCCACATGCCA	563
Db	501	GTBACAGGGAAGTCCACAGAGCCAGTCTCAATGTTCTTTGTGTGACCTCTCTTCACATACCA	560
Qy	564	CCGACACATGTAATTAAGATGTTTGTGTGAAGACCAATATGACACCACTCACCTTCACA	623
Db	561	CTTGGACCTTGAATAATGAGAGTCTTGTGTGCTGTCCACATATATACCACTTCACTTGG	620
Qy	624	CAGTCACTAGTGTGTGCAAGTGAATGCGACAGTGGCTGTACAGCTTCTCTGGGAGCTG	683
Db	621	CTACTCAGTACCTCTGTGAGGAGTGATGCCAGTGGCTGTGCATCAACTCCCCCTTAGGGCTG	680
Qy	684	AAGCTCAACCTCTTTGGACCCAGGAGACCTTACTCTGTGAGCTGTGTACGAAGAGCCAG	743
Db	681	AAGCTCAACCTCTCTGTGAGCCAGGAGACCTGTGAGCTGTGTGAATTTGAAAGGGCAGG	740
Qy	744	TGGCCACAGTTCCTTGATCCCTGGGCTGTGTTTCCACAGAGCCCTTTTGTGTGACGCCAG	803
Db	741	TAGCCAGAGCTCACTGATCTCTGGGTTGAGCTGTGCCATATAGCTTTTGTGTGACGCCGG	800
Qy	804	TAAAGGTTTGAAGGCGAGAGATGGGTTGCCCGCGAGGTATGCAATTGCCAGGGGGGTCCA	863
Db	801	TGAGAGTTGGGGGCAACACCCAGATTCAACGACAGGACATGCACTGCCAAGGAGGCTCCA	860
Qy	864	GGATGTGCTGTGCAACAAGATTTTTGTGAGACTTCGCTGATTTGGCTGGAATGACTGGA	923
Db	861	GGATGTGCTGTGCAACAAGATTTTTGTGAGACTTCGCTGATTTGGCTGGAATGACTGGA	920
Qy	924	TGATCAACCTGTAAAGGCTATGCCATGTCTGTGCACGTGGGAGTCCCATACATGTGCG	983
Db	921	TGATCAACCTGTAAAGGCTATGCCATGTCTGTGCACATAGGGGAGTCCCATACATATAG	980
Qy	984	CAGGATCCCTGGGATCTGTGCTCCCTTGCACACTGAGTGTGATCTGTGTCAAAAGCA	1043
Db	981	CAGGATCCCTGTGATGTGTGCTCCCTTGCACACTGAGTGTGATCTGTGTCAAAAGCA	1040
Qy	1044	ACCGAGCTGTGGACCACTGTGAGGGGCTGTGCTGTGCGCTTACATCTGTGGCGCCCTC	1103
Db	1041	ACACAGCTGTGGAGCACTGTGAGGGGCTGTGCTGTGATACCGAGCGCCGCGCCCTCC	1100
Qy	1104	TGCTCTTGTCTACTATGTACAGGAGACAGCAACTTGTCAAGACGATATACCTGCATGAG	1163
Db	1101	TGCTCTTGTCTACTATGTACAGGAGACAGCAACTTGTCAAGACGATATACCTGCATGAG	1160
Qy	1164	TGCGTGAAGCCCTGTGGGGGTAGTATGCTTATGGGTATACAGGCTCCGAGAGTGAATG	1223
Db	1161	TAGTGAAGGCTGTGGGTGCAATGATCTATGTGTGTGTATGGGCAAGCCCAAGTGTGATG	1220
Qy	1224	G	1224
Db	1221	G	1221
RESULT 6			
US-09-054-526B-2			
; Sequence 2, Application US/09054526B			
; Patent No. 6197550			
; GENERAL INFORMATION:			
; APPLICANT: H.TTEN, GERTTUD			
; APPLICANT: NEIDHARDT, HELGE			
; APPLICANT: BECHTOLD, ROLF			
; APPLICANT: POHL, JENS			

Query Match	13.6%	Score 212.2	DB 3	Length 265
Best Local Similarity	87.5%	Pred. No. 1.7e-55		
Matches 232	Conservative 0	Mismatches 33	Indels 0	Gaps 0
QY 925	CATCAGACCTGAAAGCCTATGCCATGAACTCTTGCACTGGGAGTGGCCACTACATGTGGC	984		
Db 1	CATCAGACCTGAAAGGCTAGGCCATGAACTCTTGCACTAGGGACATGGCCACTACATATGC	60		
QY 985	AGGCATATCCCTGGCATCTCTGCTCTCTTTCACACTGCACTGCTGAATCTGCTCAAAAGCAA	1044		
Db 61	AGGCATATCCCTGGGATATGCTGCTCTCTTTCACACTGCACTGCTGAATCTTCTCAAGGCCAA	120		
QY 1045	CGCAGCTGCGGGGACACACCTGGCAGGGGGCTGCGTCTGCTGCTTCACATCTGGGGCCCTCT	1104		
Db 121	CACAGCTGCAAGGACACCACTGGAGGGGGCTCATGCTGTGTACCCACGGGCCGGCCCCCT	180		
QY 1105	GTCCTTGCTCTACTATGACAGGAGACAGCAACATTGTCAAGCGGATATTACTTACATATGT	1164		
Db 181	GTCCTCTCTCTATTATGACAGGACAGCAACATTGTCAAGCTACATTACTTACATATGT	240		
QY 1165	GGTCGAGGCCCTCGGGGTAGTTAG 1189			
Db 241	AGTAGAGGCTCTGGGTGCAATTAG 265			

Query Match	13.6%	Score 212.2	DB 4	Length 265
Best Local Similarity	87.5%	Pred. No. 1.7e-55		
Matches 232	Conservative	0	Mismatches 33	Indels 0
				Gaps 0
QY 925	CATCCAGCCGGAAGGCTATGCCATGACTTCTGCACCTGGGAGTAGTGCCCACTACATGTGGC			984
Db 1	CATCCAGCCGGAAGGCTATGCCATGACTTCTGCACCTGGGAGTAGTGCCCACTACATGATGC			60
QY 985	AGGCATGCGCTGGCATCTGTGCCTCTTTCACACTGCAGTGGCTGAATGTGCTCAAAAGCCAA			1044
Db 61	AGGCATGCGCTGGCATCTGTGCCTCTTTCACACTGCAGTGGCTGAATGTGCTCAAAAGCCAA			120
QY 1045	CGGAGCTGTGTGGACCACTGCGAGGGGCTCTGCGTGGATGCTTCATCTGTGGGGCCCTCT			1104
Db 121	CACAGCTGCGAGGACCACTGAGGGGGCTCATGTGTGTATCCACAGGGCCGGGGCCCTCT			180
QY 1105	GCTTTTGCTCTACTATGACAGGGAGACGAATTTGTCAAGAGGATTTACCTGACATGGT			1164

Db 181 GTCCTCTCTATTATATACAGAGGACACCAACATTTGTCAAGACTGACTTACTTACTGACATGTT 240

QY 1165 GGTGAGGCGCTGCGGCTGTAGTTAG 1189

Db 241 AGTAGAGGCGCTGTGGGTGCAAGTTAG 265

RESULT 9

US-08-455-550-2
Sequence 2, Application US/08455550
Patent No. 5670338
GENERAL INFORMATION:
APPLICANT: MURAKAMI, KAZUO
APPLICANT: UENO, NAOTO
APPLICANT: KATO, YUKIO
TITLE OF INVENTION: XENOPUS LAEVIS BONE MORPHOGENETIC PROTEINS AND USE THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, Bronsteijn, Roberts & Cushman
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

Query Match	9.2%	Score 143.4	DB 1	Length 687	.
Best Local Similarity	61.7%	Pred. No. 3.3e-34			
Matches 266	0	Mismatches 156		Indels 9	Gaps 2

Oy	832	CCGGGAGAGTTCGATTTCCACAGGGGGGCTCCAGATGCTGTGCACAAAGTTTATGT	891
Db	127	AAGGAGAGCTTAACTGTGATCAGAACTCCAAATCTGTCTGTAGGAAAGCTATTATGT	180
Oy	892	AGACTCCGTGAGATGCTGGAATGACTGGATCATCCAGCTGAAGGCATTCGCATGAA	951

Accession	Sequence	Length
Db 187	AGACCTCAGAGATTTGCGGTGTAATGATGATTTAAAAAACGAGGGATTCAGATAAA	246
Qy 952	CTTGTGACATGGGAGAGGCCCACTACATGAGAGCATGCTGGCATCTCGCCCTCT	1011
Db 247	TATATGATGGGCTTTTGCCCAATGCAATTCCTGAGGCCCAAGTAGGAGAGCTTCAT	306
Qy 1012	TGCACATGCAGTGTGTAATCTGCTCAAAAGCAACGACAGCTGCTGGACACACTGCCAGGG	1071
Db 307	CCACACACAGGATTAATTAATCTCATTTAAGGCCAAC-----AATATCCAGACAGCAGTAA	360
Qy 1072	CTGTGCTGGGTGCTCATCTGAGGGGCCCTGCTTGTGCTCATGACAGGAGACAG	1131
Db 361	CTCATGCTGTGCTCTACCAAAAGGGCCCTTTGTCCATGCTTTACTTTGATAGAAATAA	420
Qy 1132	CACATTTGTCAGAGCGGATATACCTGACATGATGTGAGAGGCTCGGGCTTAGTTAACT	1191
Db 421	CACGTTCTCAGACACTGACATTCGATGATGATTTGGAGAGGCTGTGGCTCTACCTAGG	480
Qy 1192	TATGGTGATTA 1202	
Db 481	CTTGGCTACA 491	

RESULT 10
ME-09-765

05-08-765-662-13
Sequence 13, Application US/08765662
Patent No. 5929213
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:

STREET: 4225 Executive Square, Suite 1400
 CITY: LA JOLLA
 STATE: CA
 COUNTRY: US
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: Windows95
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/184.933
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/274.215
 FILING DATE: 13-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Hallie, Ph.D., Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07265/040001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-678-5070
 TELEFAX: 619-678-5099
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 360 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 1...357
 US-09-184-933-11

Query Match 8.7%: Score 136; DB 3; Length 360;
 Best Local Similarity 62.8%; Pred. No. 4.3e-32;
 Matches 230; Conservative 0; Mismatches 130; Indels 6; Gaps 1;

QY 824 CGGGTTCGCCGCGAGGATGATGATGCGAGGGGGTCCAGATGCTGTGACAAAGAG 883
 DB 1 CGGGCCAG 60
 QY 884 TTTTGTAGACTTCCTGAGATGCTGGAATGACTGATCATTCAGAGCTTGAAGCTAT 943
 DB 61 CATTAAGTACCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 QY 944 GCCATGAATCTTGCAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1003
 DB 121 CAGCTGAATTAAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 QY 1004 GCTTCCTTACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1063
 DB 181 GCTCTTTTCAATTCCTGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 234
 QY 1064 GCGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123
 DB 235 GCGAGTACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 294
 QY 1124 AGGAGACGAACATTTGTCAGAGAGAGATATACCTGACATGCTGAGAGAGAG 1183
 DB 295 CATTAATGCAATGTGTCAAGAGAGATGTGCAAGATATGTGTGTGAGAGAGAG 354
 QY 1184 AGTTAG 1189
 DB 355 AGCTAG 360

RESULT 15
 PCT-US95-08745-11
 Sequence 11, Application PC/TUS9508745
 GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 4225 Executive Square, Suite 1400
 CITY: LA JOLLA
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/08745
 FILING DATE: 12-JUL-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Hallie, Ph.D., Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07265/042W01 (FD-3830)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-678-5070
 TELEFAX: 619-678-5099
 TELEX:
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 360 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 1...357
 OTHER INFORMATION:
 PCT-US95-08745-11

Query Match 8.7%: Score 136; DB 5; Length 360;
 Best Local Similarity 62.8%; Pred. No. 4.3e-32;
 Matches 230; Conservative 0; Mismatches 130; Indels 6; Gaps 1;

QY 824 CGGGTTCGCCGCGAGGATGATGATGCGAGGGGGTCCAGAGATGCTGTGACAAAGAG 883
 DB 1 CGGGCCAG 60
 QY 884 TTTTGTAGACTTCCTGAGATGCTGGAATGACTGATCATTCAGAGCTTGAAGCTAT 943
 DB 61 CATTAAGTACCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 QY 944 GCCATGAATCTTGCAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1003
 DB 121 CAGCTGAATTAAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 QY 1004 GCTTCCTTACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1063
 DB 181 GCTCTTTTCAATTCCTGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 234
 QY 1064 GCGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123
 DB 235 GCGAGTACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 294
 QY 1124 AGGAGACGAACATTTGTCAGAGAGAGATATACCTGACATGCTGAGAGAGAG 1183
 DB 295 CATTAATGCAATGTGTCAAGAGAGATGTGCAAGATATGTGTGTGAGAGAGAG 354
 QY 1184 AGTTAG 1189

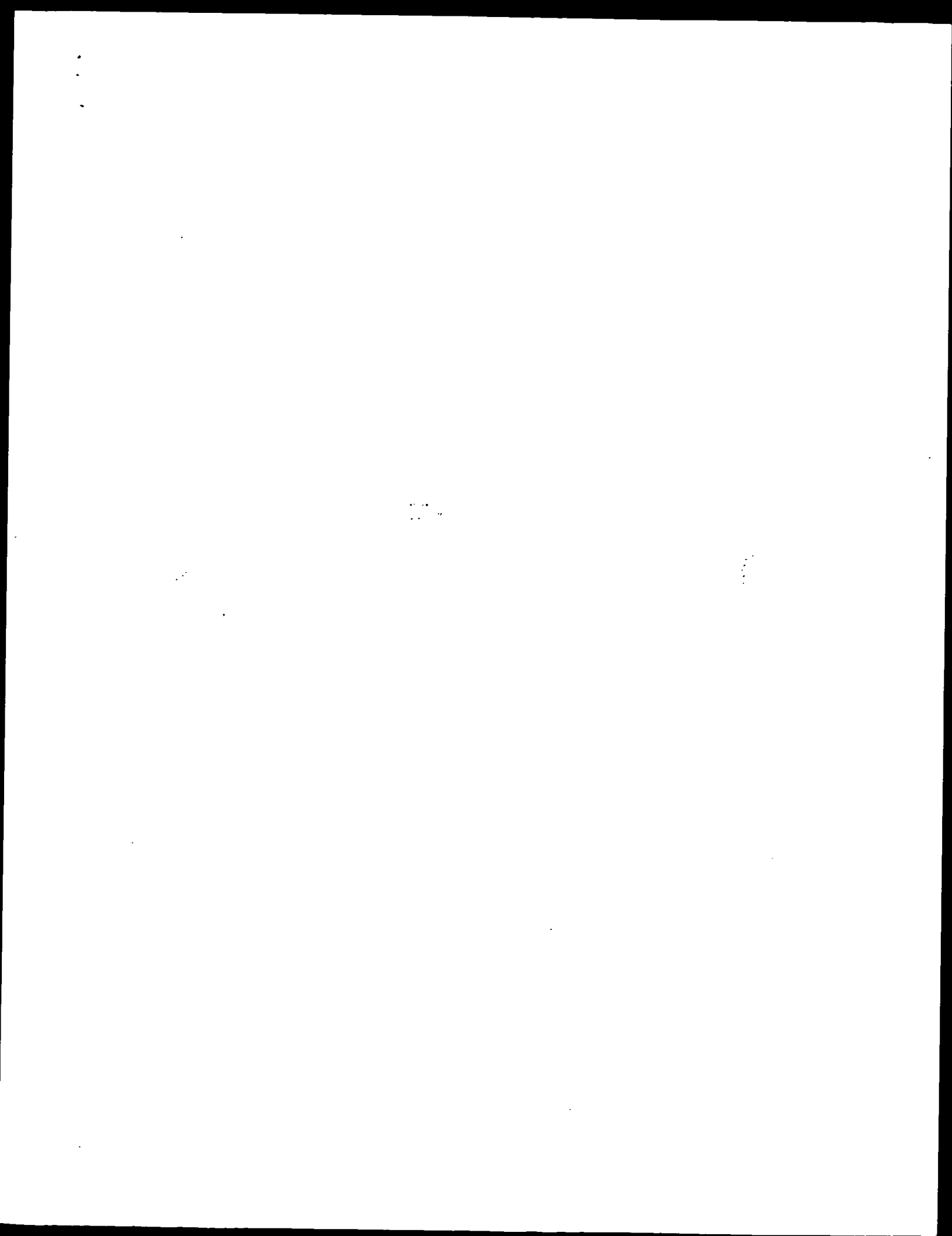
Tue Oct 15 13:49:42 2002

us-09-684-383-3.rni

Page 13

Db 355 AGCTAG 360

Search completed: October 11, 2002, 22:15:27
Job time : 47.2042 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2002, 22:15:08; Search time 1258.6 Seconds
(without alignments)
16707.608 Million cell updates/sec

Title: US-09-684-383-3

Perfect score: 1558
Sequence: 1 AAGAGTCATCCAGTCGCA.....ATGCCCTTACGTCTCCCTT 1558

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estlin: *
4: em_estmu: *
5: em_estcov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_estl: *
10: gb_estcd: *
11: gb_hic: *
12: gb_gsa: *
13: em_gsa_hum: *
14: em_gsa_liv: *
15: em_gsa_pln: *
16: em_gsa_vrt: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	752.2	48.3	941	10	B1148079 602912428
2	726.6	46.6	829	10	B1239959 602980519
3	716.8	46.0	893	10	B1246740 602959660
4	714	45.8	841	10	B1145698 602909844
5	706.6	45.4	758	10	B1128115 602879264
6	696	44.7	823	10	BF533960 602075120
7	653.8	42.0	816	10	BF322704 602023292
8	643.6	41.3	975	10	BF533968 602075129
9	509	32.7	636	10	BF326906 602026526
10	413.2	26.5	1011	11	BC020693 Homo sapi
11	299.6	19.2	493	9	AA237913
12	261.2	16.8	312	9	A1287120 u171g11.y
13	252	16.2	541	10	BC566943 602589447
14	145	9.3	445	9	A1452079 mm08a04.x
15	138.4	8.9	314	9	AA242421
16	133	8.5	586	12	BH275857 CH230-23P
17	127.2	8.2	714	10	B1152811 602917943

18	119	7.6	367	10	BG713244	BG713244 p9lin.pk0
19	116.4	7.5	546	10	BF061329	BF061329 7j51a07.x
20	116.4	7.5	555	10	BF083319	BF083319 NC1-CT024
21	116.4	7.5	627	9	A1800922	A1800922 w914e09.x
22	116.4	7.5	634	10	BF000451	BF000451 7h29c04.x
23	116	7.4	757	10	BF052102	BF052102 603378586
24	115.2	7.4	497	9	A1433268	A1433268 t132g04.x
25	114.8	7.4	558	10	BE506007	BE506007 dc18b06.y
26	114.6	7.4	504	10	BM219131	BM219131 C0920E09-
27	114.6	7.4	526	10	BF508647	BF508647 UI-H-B14-
28	112.2	7.2	493	9	A1753619	A1753619 c13a06.x
29	111	7.1	667	10	BF696144	BF696144 603345983
30	110.2	7.1	982	10	BF689098	BF689098 602185171
31	109.4	7.0	516	9	AU157212	AU157212 AU157212
32	107.8	6.9	372	10	BF542340	BF542340 UI-R-C3-s
33	107	6.9	389	9	AW385664	AW385664 PM3-LT003
34	104.8	6.7	535	9	AU157878	AU157878 AU157878
35	103.2	6.6	942	10	BF309695	BF309695 601891832
36	101.8	6.5	601	9	BB667192	BB667192 BB667192
37	101.4	6.5	401	10	BG995292	BG995292 CM0-HT129
38	99.8	6.4	831	12	CNS02TTF	AL213320 Tetradon
39	99	6.4	920	12	CNS03ELX	AL240559 Tetradon
40	98.8	6.3	669	9	BI646826	BI646826 603276766
41	98.4	6.3	515	9	AA587288	AA587288 n074e05.s
42	98	6.3	493	10	BF000351	BF000351 7h26g10.x
43	95.8	6.1	623	9	AW911189	AW911189 ur83c08.y
44	94.4	6.1	368	10	BI961669	BI961669 MON01-3-A
45	94.4	6.1	401	10	BI960944	BI960944 MON01-3-A

ALIGNMENTS

RESULT 1
B1148079
LOCUS 602912428P1 NC1_CGAP_L19 Mus musculus cDNA clone IMAGE:5053471 5', mRNA sequence.
DEFINITION B1148079.1 GI:14608080
ACCESSION B1148079
VERSION B1148079.1
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 941)
AUTHORS Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
TITLE NIH-MGC http://mgc.ncl.nih.gov/.
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M1145 row: 9 column: 08
High quality sequence stop: 887.
Location/Qualifiers
1..941
/organism="Mus musculus"
/strain="FVB/N"
/cd_xref="taxon:10090"
/clone="IMAGE:5053471"
/clone_id="NC1_CGAP_L19"
/lab_host="DH10B (rt phage-resistant)"
/note="Organ: Liver; Vector: pCMV-SPORT6; Site:1; NOTI; Site:2; Salt: Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NC1_CGAP Library."

BASE COUNT

202 a 260 c 246 g 233 t

ORIGIN

Query Match 48.3%; Score 752.2; DB 10; Length 941;
 Best Local Similarity 95.1%; Pred. No. 6.2e-199;
 Matches 874; Conservative 0; Mismatches 33; Indels 12; Gaps 9;

QY 650 GCCAGTGGCTGTACACAGCTTCTCTGGG-ACCTGAAGCTCAAGCTCTTGCAGCCAGG 708
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 DB 1 GCCAGTGGCTGTACACAGCTTCTCTGGG-ACCTGAAGCTCAAGCTCTTGCAGCCAGG 59

QY 709 AACCTTACTGAGGAGGTGACAGAAAGCAGAGTGGCCACAGTCTTGTATCTGGG 768
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 DB 60 AACCTTACTGAGGAGGTGACAGAAAGCAGAGTGGCCACAGTCTTGTATCTGGG 119

QY 769 CTGATTTCCACAGAGCTTTGTGGAGCCAGAGTAAAGGTTGAGGGCAAGCATGGGT 828
 |||||||
 DB 120 CTGATTTCCACAGAGCTTTGTGGAGCCAGAGTAAAGGTTGAGGGCAAGCATGGGT 179

QY 829 TCCCGGCGAGGATTCATTTCCAGAGGGGGTCCAGAGTGTCTGTGCAGACAGTCTTT 888
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 DB 180 TCCCGGCGAGGATTCATTTCCAGAGGGGGTCCAGAGTGTCTGTGCAGACAGTCTTT 238

QY 889 TGTAACTTCCGTAGATTGGCTGAATGATGGATCATAGAGCTGAAGCTTATCCAT 948
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 DB 239 GGTAACTTCCGTAGATTGGCTGAATGATGGATCATAGAGCTTATCCAT 298

QY 949 GAACCTTGCAGCTGGGAGTGGCCACATGATGAGGAGCATGCTGGCATCTGCTCTC 1008
 |||||||
 DB 299 GAACCTTGCAGCTGGGAGTGGCCACATGATGAGGAGCATGCTGGCATCTGCTCTC 358

QY 1009 CTTTACACAGCTGCTGATGCTGCTCAAGAGCAAGCAGCTGCTGGCAGCAGCTGGCAG 1068
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 DB 359 CTTTACACAGCTGCTGATGCTGCTCAAGAGCAAGCAGCTGCTGGCAGCAGCTGGCAG 418

QY 1069 GGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1128
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 DB 419 GGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 478

QY 1129 CAGCAAGATGTCAGAGGAGTATACCTGATGATGATGATGATGATGATGATGATGAT 1188
 |||||||
 DB 479 CAGCAAGATGTCAGAGGAGTATACCTGATGATGATGATGATGATGATGATGATGAT 538

QY 1189 GCTTATGGGATACAGAGCTGCTGAGTGAATGCTTCCAGAGGAA-GGGAAAGCT 1247
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 DB 539 GCTTATGGGATACAGAGCTGCTGAGTGAATGCTTCCAGAGGAAAGCT 598

QY 1248 GTTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1307
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 DB 599 GTTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 658

QY 1308 CTTGAGGAGTGCAGCTCTTAAAGAGTACATGATGATGATGATGATGATGATGATGAT 1367
 |||||||
 DB 659 CTTGAGGAGTGCAGCTCTTAAAGAGTACATGATGATGATGATGATGATGATGATGAT 718

QY 1368 GACATGGTGAAGCAGTACAGCAGCTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1423
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 DB 719 GACATGGTGAAGCAGTACAGCAGCTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 778

QY 1424 CTGAT 1481
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 DB 779 CTGAT 838

QY 1482 TGTAACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1539
 |||||||
 DB 839 TGTAACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 898

QY 1540 TGCCTTAAGTGTCTCCCTT 1558
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 DB 899 TGCCTTAAGTGTCTCCCTT 917

RESULT 2
 B1329959

LOCUS B1329959 829 bp mRNA linear EST 30-JUL-2001
 DEFINITION 602980519F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5133317 5',
 mRNA sequence.
 ACCESSION B1329959
 VERSION B1329959.1 GI:15014616
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
 1 (bases 1 to 829)
 NIH-MGC <http://mgs.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 TITLE
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLNL1327 row: f column: 06
 High quality sequence stop: 789.
 Location/Qualifiers
 1..829
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5133317"
 /clone_lib="NCI_CGAP_L19"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: Liver; Vector: pCMV-Sport6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.9 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 187 a 246 c 217 g 179 t
 ORIGIN

Query Match 46.6%; Score 726.6; DB 10; Length 829;
 Best Local Similarity 97.5%; Pred. No. 8.1e-192;
 Matches 791; Conservative 0; Mismatches 14; Indels 6; Gaps 5;

QY 1 AAGAGTATGTCAGTGGAGTCACTGATCTCCAGGCTCCGAGGCCAGAC 60
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 DB 22 AAGAGTATGTCAGTGGAGTCACTGATCTCCAGGCTCCGAGGCCAGAC 81

QY 61 AGAGTTGAAG-CAGTCCCTGAGACCTGGAATATAGCTTTGGTCTTAAAGAGCT 119
 |||||||
 DB 82 AGAGTTGAAGCCACTCCCTGAGACCTGGAATATAGCTTTGGTCTTAAAGAGCT 141

QY 120 ATCCCTCAGCAATGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 179
 |||||||
 DB 142 ATCCCTCAGCAATGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 201

QY 180 TACTGAACCCCAAACTGAGGCTCCATGAGCAGATGTTGGGGTGCATCTTTGACCTGG 239
 |||||||
 DB 202 TACTGAACCCCAAACTGAGGCTCCATGAGCAGATGTTGGGGTGCATCTTTGACCTGG 261

QY 240 AGAGCCAGGAGGAGTGTCTGATTTGGCCAGAAAGTATCTCGACAGCTGACG 299
 |||||||
 DB 262 AGAGCCAGGAGGAGTGTCTGATTTGGCCAGAAAGTATCTCGACAGCTGACG 321

QY 300 TCAGCCAGGCGCCCAATGATGAGTGGCCAGTGCAGAGGGGCTCAAGACCGCGCTGC 359
 |||||||
 DB 322 TCAGCCAGGCGCCCAATGATGAGTGGCCAGTGCAGAGGGGCTCAAGACCGCGCTGC 381

QY 360 AAGGCTCCGCGGCGCTGAGCGGAAACCTGTTGAGCATGACAGACAGCAAGAAAT 419
 |||||||
 DB 382 AAGGCTCCGCGGCGCTGAGCGGAAACCTGTTGAGCATGACAGACAGCAAGAAAT 441

QY 420 ATGAGATCATGCTTTGCTGACACAGACCTCTCCAGCATCAACAGACCGCGCTGAGT 479

Db 442 ATGAGTATCTGCTGTCAGACAGACCTCTCCAGCTCAACACAGCCGCTGAGT 501
 480 TCCACTTCTCTGTAGATAGCCAGTGGATGAGATCCGAGACCCGCTTCATGTTCT 539
 Db 502 TCCACTTCTCTGTAGATAGCCAGTGGATGAGATCCGAGACCCGCTTCATGTTCT 561
 Qy 540 TCGTGCAGTTCCCGCCAGTATGCCAGCCAGACCATGATATTAAGAGTTCTTGTCTAAGAC 599
 Db 562 TCGTGCAGTTCCCGCCAGTATGCCAGCCAGACCATGATATTAAGAGTTCTTGTCTAAGAC 621
 Qy 600 CATATGACACCAACCTGACCTTGACAGTACAGTGGTGGAGTGGATGGCAGTGGCT 659
 Db 622 CATATGACACCAACCTGACCTTGACAGTACAGTGGTGGAGTGGATGGCAGTGGCT 679
 Qy 660 GGTACACAGCTTCTCTGAGCTGAGCTCAAGCTCTTGCAGCCAGGACACCTTACTC 719
 Db 680 GGTACACAGCTTCTCTGAGCTGAGCTCAAGCTCTTGCAGCCAGGACACCTTACTC 739
 Qy 720 TGGAGCTGTACCAAGACCAAGTGGCCAGAGTTCCTTATCTCTGGCTGGTTTCC 779
 Db 740 TGGAGCTGTACCAAGACCAAGTGGCCAGAGTTCCTTATCTCTGGCTGGTTTACC 797
 Qy 780 ACAGGCTTTTGTGGCAGCCAGTAAAGCT 810
 Db 798 ACAGGCC-TTGTGGCAGCCAGTAAAGCT 827

RESULT 3
 LOCUS B1246740 893 bp mRNA linear EST 17-JUL-2001
 DEFINITION 602959660P1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:512587 5',
 mRNA sequence.
 ACCESSION B1246740
 VERSION B1246740.1 GI:14790995
 KEYWORDS EST
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

REFERENCE NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ULNL at:
 http://image.llnl.gov

FEATURES

source

Plate: LMAN1306 row: 9 column: 16
 High quality sequence stop: 778.
 Location/Qualifiers
 1..893

/organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:512587"
 /clone_lib="NCI_CGAP_L19"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: liver; Vector: pcMV-Sport6; Site_1: NotI;
 Site_2: SalI; cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.9 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 196 a 259 c 242 g 196 t

Query Match 46.0% Score 716.8; DB 10; Length 893;
 Best Local Similarity 96.0% Pred. No. 4,6e-189;
 Matches 854; Conservative 0; Mismatches 22; Indels 14; Gaps 11;

Qy 95 AGGCTTTGGCTCTTTTAAGAGGCTATCTCCAGCAATGGCTCTCTCTGCT 154
 Db 1 AGGCTTTGGCTCTTTTAAGAGGCTATCTCCAGCAATGGCTCTCTCTGCT 60
 Qy 155 CTTCCTGTTCTGACCTCAACCAAGTACTGAACCCCAAACTGAGAGTTCATGCCCCA 214
 Db 61 CTTCCTGTTCTGACCTCAACCAAGTACTGAACCCCAAACTGAGAGTTCATGCCCCA 120
 Qy 215 TGTGGGGTGCATCTTTGACCTGGAGAGCCAGGAGGAGTGTCTCTGATTTGGCCAA 274
 Db 121 TGTGGGGTGCATCTTTGACCTGGAGAGCCAGGAGGAGTGTCTCTGATTTGGCCAA 180
 Qy 275 AAAAGTATCTGAGACAACTGCACTGACAGCCAGCCCATATCTAGTGGCCAGTGC 334
 Db 181 AAAAGTATCTGAGACAACTGCACTGACAGCCAGCCCATATCTAGTGGCCAGTGC 240
 Qy 335 AGAGGGGCTCTCAACAGCGGCTGAGGCGCTCCGGGGCTCCAGCGGAAACCTGTG 394
 Db 241 AGAGGGGCTCTCAACAGCGGCTGAGGCGCTCCGGGGCTCCAGCGGAAACCTGTG 300
 Qy 395 GAGCATGACAGAGACAGAAATATGATCATCAGCTTGTGACAGACAGCTTCC 454
 Db 301 GAGCATGACAGAGACAGAAATATGATCATCAGCTTGTGACAGACAGCTTCC 360
 Qy 455 AGCATCAACAGACCCGCTCAGTTCACCTTCTGCTAGAG - ATGGCAGTGGCATGA 513
 Db 361 AGCATCAACAGACCCGCTCAGTTCACCTTCTGCTAGAG - ATGGCAGTGGCATGA 420
 Qy 514 GGTCCGGCAGACCCGCTCAGTTCACCTTCTGCTAGAG - ATGGCAGTGGCATGA 573
 Db 421 GGTCCGGCAGACCCGCTCAGTTCACCTTCTGCTAGAG - ATGGCAGTGGCATGA 480
 Qy 574 GAATATTAAGAGTCTTGTGCTATGACATATGACACCAACCTTGGCAAGTCACTA 633
 Db 481 GAATATTAAGAGTCTTGTGCTATGACATATGACACCAACCTTGGCAAGTCACTA 540
 Qy 634 CGTGTG-TGCAGTGAATGCACTGCTGCTGACACCTTCTCTGGAGCCTGAAGTCAAG 692
 Db 541 CGTGTG-TGCAGTGAATGCACTGCTGCTGACACCTTCTCTGGAGCCTGAAGTCAAG 600
 Qy 693 CTGCTTGCAGCCAGGAGACCTTACTGTGG - AGCTGATACCAAGAAAGCCAGTGGCCA - 750
 Db 601 CTGCTTGCAGCCAGGAGACCTTACTGTGG - AGCTGATACCAAGAAAGCCAGTGGCCA - 660
 Qy 751 CAGTTCCTTGAATCTGAGGCTGCTTCCACAGGCTTGTGGAGCCAGTAAAGGT 810
 Db 661 CAGTTCCTTGAATCTGAGGCTGCTTCCACAGGCTTGTGGAGCCAGTAAAGGT 720
 Qy 811 T--GAGGCGAAGCAATC--GAGTTCGCCGCGAGGATATCG--ATTGCGAGGGGGTCCAG 864
 Db 721 TTAGAGGGGCAACATCCGCGGTTCCCGCGCAAGTATTCGAATTCAGAGGGGCTCCAG 780
 Qy 865 GA-TGTGCTGTGACAAAGATTTTGTAGACTTCGATGAGATTGGCTGATGAC-TGG 922
 Db 781 GATTTGCTGTGACAAAGATTTTGTAGACTTCGATGAGATTGGCTGATGAC-TGG 840
 Qy 923 ATCATTCACCTGGAAGGCTATGCAATCTTCTGCACTGGGCAATGGCC 972
 Db 841 ATCATTCACCTGGAAGGCTATGCAATCTTCTGCACTGGGCAATGGCC 888

RESULT 4

B1145698

LOCUS B1145698 841 bp mRNA linear EST 05-JUL-2001
 DEFINITION 602909844P1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5050810 5',
 mRNA sequence.
 ACCESSION B1145698
 VERSION B1145698.1 GI:14605699
 KEYWORDS EST
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Query Match 46.0% Score 716.8; DB 10; Length 893;
 Best Local Similarity 96.0% Pred. No. 4,6e-189;
 Matches 854; Conservative 0; Mismatches 22; Indels 14; Gaps 11;

REFERENCE 1 (bases 1 to 841)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L1AM1138 row: h column: 11
 High quality sequence stop: 835.
 Location/Qualifiers

FEATURES
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 /organism="Mus musculus"
 /strain="FVB/N"
 /db.xref="taxon:10090"
 /clone="IMAGE:5050810"
 /lab_host="NCL_CGAP_L19"
 /note="Organ: Liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCL_CGAP Library."
 BASE COUNT 181 a 238 c 221 g 201 t
 ORIGIN

Query Match 45.8%; Score 714; DB 10; Length 841;
 Best Local Similarity 97.1%; Pred. No. 2,7e-188;
 Matches 812; Conservative 0; Mismatches 15; Indels 9; Gaps 8;

678 GACCTGAAGCTCAGAGCTCTTGCAGCCAGGACACTTACTCTGAGCTGTACAGAAA 737
 1 GACCTGAAGCTCAGAGCTCTTGCAGCCAGGACACTTACTCTGAGCTGTACAGAAA 59
 738 GCCAGGTGGCCACAGTCTCTTGAATCCTGGGCTGGTTTCCACAGGCTTTTGGCAG 797
 60 GCCAGGTGGCCACAGTCTCTTGAATCCTGGGCTGGTTTCCACAGGCTTTTGGCAG 119
 798 CCCAGGTGAAGGTTGAGGGCAAGCATCGGGTCCCGCGAGATGATGATGCCAGGGG 857
 120 CCCAGGTGAAGGTTGAGGGCAAGCATCGGGTCCCGCGAGATGATGATGCCAGGGG 179
 858 GGTCCAGATGCTGCTGCTGCAAGAGTTTGTAGACTTCCGTGAGATTGGCTGAATG 917
 180 GGTCCAGATGCTGCTGCTGCAAGAGTTTGTAGACTTCCGTGAGATTGGCTGAATG 239
 918 ACTGATCATCAGCAGCTGAAGGCTATGCGATGAATCTCTGACATGGGAGAGGCCATAC 977
 240 ACTGATCATCAGCAGCTGAAGGCTATGCGATGAATCTCTGACATGGGAGAGGCCATAC 299
 978 ATGTGGCAGGATCGCTGCTGCTGCTCTTTCACACTGACAGTCTGTAATCTGCTCA 1037
 300 ATGTGGCAGGATCGCTGCTGCTGCTCTTTCACACTGACAGTCTGTAATCTGCTCA 359
 1038 AAGCCAAAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1097
 360 AAGCCAAAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419
 1098 GCCCTCTCTTTTCTCTACTATGACAGGAGCAGCAATTTGTCAGAGGATATACCTG 1157
 420 GCCCTCTCTTTTCTCTACTATGACAGGAGCAGCAATTTGTCAGAGGATATACCTG 479
 1158 ACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1217
 480 ACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 539
 1218 AGAATGGCTTCTCTGAGAA-GGGAAACTCTGTTCCACTTCTGTCAGAAATGGAACAC 1276

Db 540 AGAATGGCTTCTCTGAGAAAGGAGAAACTCTGTTCCCACTTCTGTCAGAAATGGAACAC 599
 QY 1277 CTTTCTAGATGATGACATCCCTCTGTGACTTTCAGGGGATTCACCTCTGAA-AGAGACT 1335
 Db 600 CTTTCTAGATGATGACATCCCTCTGTGACTTTCAGGGGATTCACCTCTGAAAGAGACT 659
 QY 1336 CACTAGTACACACAGCTTCTCTCTCCGAGCAAT-GGTTAGCCAGTACACCATCC 1394
 Db 660 CACTAGTACACACAGCTTCTCTCTCCGAGCAATGGTTAGCAGGATACACCATCC 719
 QY 1395 TCAGCCTTAAGTTAGAGGCTAATTCAC--TCCTACATATATATGATGATTTTCTCAGCA 1452
 Db 720 TCAGCCTTAAGTTAGAGGCTAATTCACAGGCTTACCAAGCAATGATGATTTTCTCAGCA 779
 QY 1453 AACAC-CCCTTACTCT-CCCTTACTACATATGATGATGATGATGATGATGATGATG 1506
 Db 780 AACACCCCTTACTCTCTCTTACTGATGATGATGATGATGATGATGATGATGATG 834

RESULT 5
 LOCUS B1328115 758 bp mRNA linear EST 30-JUL-2001
 DEFINITION 602979264F1 NCL_CGAP_L19 Mus musculus cDNA clone IMAGE:5132391 5', mRNA sequence.
 ACCESSION B1328115
 VERSION B1328115.1 GI:15012772
 KEYWORDS EST
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 758)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L1AM11324 row: o column: 16
 High quality sequence stop: 758.
 Location/Qualifiers

FEATURES
 Source 1..758
 /organism="Mus musculus"
 /strain="FVB/N"
 /db.xref="taxon:10090"
 /clone="IMAGE:5132391"
 /lab_host="NCL_CGAP_L19"
 /note="Organ: Liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCL_CGAP Library."
 BASE COUNT 168 a 229 c 194 g 167 t
 ORIGIN

Query Match 45.4%; Score 706.6; DB 10; Length 758;
 Best Local Similarity 98.4%; Pred. No. 3e-186;
 Matches 745; Conservative 0; Mismatches 9; Indels 3; Gaps 3;

QY 40 AGGTCCTGCTGCTCCAGAGAGAGTTGAAG-CATTCCTGAGACCTGATATATAGGC 98
 Db 1 AGGTCCTGCTGCTCCAGAGAGAGTTGAAGCACTCCGTTGAGACCTGATATATAGGC 60
 QY 99 TTTGGGCTCTTAAAGAGGATATCTCCAGCAATGGCTCTCTGCTGCTGCTGCTGCT 158
 Db 61 TTTGGGCTCTTAAAGAGGATATCTCCAGCAATGGCTCTCTGCTGCTGCTGCTGCT 120

OY 159 TGTTCCTGACTCAACACACAGTGTGAACCCCAAACTGAGGTCATGCCAGCATGTT 218
 DB 121 TGTTCCTGACTCAACACACAGTGTGAACCCCAAACTGAGGTCATGCCAGCATGTT 180
 OY 219 GGGGTGACATCTTTGACCTGAGAGAGCCGCGGAGCTCTTCTGATTTGGCCAGAAAA 278
 DB 181 GGGGTGACATCTTTGACCTGAGAGAGCCGCGGAGCTCTTCTGATTTGGCCAGAAAA 240
 OY 279 GTATCTCTGACAAAGTGTGACCTGAGAGAGCCGCGGAGCTCTTCTGATTTGGCCAGAG 338
 DB 241 GTATCTCTGACAAAGTGTGACCTGAGAGAGCCGCGGAGCTCTTCTGATTTGGCCAGAG 300
 OY 339 GGGCTCTCAAGACCCGCTGAGAGAGCCGCGGAGCTCTTCTGATTTGGCCAGAG 398
 DB 301 GGGCTCTCAAGACCCGCTGAGAGAGCCGCGGAGCTCTTCTGATTTGGCCAGAG 360
 OY 399 ATGACCCAGAGACAGACAAATATGAGATCATGACCTTTGCTGACACAGACCTCTCCAGCA 458
 DB 361 ATGACCCAGAGACAGACAAATATGAGATCATGACCTTTGCTGACACAGACCTCTCCAGCA 420
 OY 459 TCAACCAAGACCCGCTGAGAGAGCCGCGGAGCTCTTCTGATTTGGCCAGAG 518
 DB 421 TCAACCAAGACCCGCTGAGAGAGCCGCGGAGCTCTTCTGATTTGGCCAGAG 480
 OY 519 GGCAGACCCGCTGAGAGAGCCGCGGAGCTCTTCTGATTTGGCCAGAG 578
 DB 481 GGCAGACCCGCTGAGAGAGCCGCGGAGCTCTTCTGATTTGGCCAGAG 540
 OY 579 TAAAGATCTTGTGCTTAAGACCAATATGACCAACCTTCAGTCAAGTCAAGTCAAGTCAAG 638
 DB 541 TAAAGATCTTGTGCTTAAGACCAATATGACCAACCTTCAGTCAAGTCAAGTCAAGTCAAG 600
 OY 639 TGCAGTGAATGCGAGTGGCTGAGAGAGCCGCGGAGCTCTTCTGATTTGGCCAGAG 698
 DB 601 TGCAGTGAATGCGAGTGGCTGAGAGAGCCGCGGAGCTCTTCTGATTTGGCCAGAG 660
 OY 699 GCAGCAGGAGACACCTTACTGAGTGTGACAG-AAAACAGAGTGGCCAGAGTTC 757
 DB 661 GCAGCAGGAGACACCTTACTGAGTGTGACAG-AAAACAGAGTGGCCAGAGTTC 720
 OY 758 TTGATCTCTGGCT-GGTTTTCCACAGGCTTTTGTG 793
 DB 721 TTGATCTCTGGCTGGCTTTTCCACAGGCGCTTTTGTG 757
 RESULT 6
 BF533960 823 bp mRNA linear EST 11-DEC-2000
 LOCUS 602075120P1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:4212125 5'
 DEFINITION mRNA sequence.
 ACCESSION BF533960
 VERSION BF533960.1 GI:11621323
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 823)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaab-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM9782 row: 9 column: 06
 High quality sequence stop: 754.
 Location/Qualifiers

source 1. 823
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4212125"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: Liver; Vector: pCMV-Sport6; Site: 1; NCI;
 Site: 2; Salt: Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.9 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP library."
 BASE COUNT 181 a 247 c 221 g 174 t
 ORIGIN
 Query Match 44.7% Score 696; DB 10; Length 823;
 Best Local Similarity 96.6%; Pred. No. 2.9e-183;
 Matches 786; Conservative 0; Mismatches 20; Indels 8; Gaps 7;
 OY 46 CCTGTGCGCCAGAGAGAGTTGAG-CACCTCCCTTGAGACCTGAAATATAGCTTTGG 104
 DB 4 CCGTGGCCCGAGAGAGAGTTGAGAGCCATCCGTTGAGACCTGAAATATAGG 62
 OY 105 TCCCTTAAGAGAGCTATCTCCAGCAATGCTCTCTCTGCTCTCTCTCTCTCTCC 164
 DB 63 TCCCTTAAGAGAGCTATCTCCAGCAATGCTCTCTCTCTCTCTCTCTCTCTCTCC 122
 OY 165 TGACGTCAACCACTATGTAACCCCAAACTGAGGGTCCATGCCAGATGTTGGGGTG 224
 DB 123 TGACGTCAACCACTATGTAACCCCAAACTGAGGGTCCATGCCAGATGTTGGGGTG 182
 OY 225 CCATCTTTGACCTGAGAGAGCCAGCGGAGCTGCTTCTGATTTGGCCAGAAAGTATCC 284
 DB 183 CCATCTTTGACCTGAGAGAGCCAGCGGAGCTGCTTCTGATTTGGCCAGAAAGTATCC 241
 OY 285 TGGACAGCTGACCTCAAGCAGCGCCCGCCACTACTAGTCCGCGCAGTCCAGAGGGCTC 344
 DB 242 TGGACAGCTGACCTCAAGCAGCGCCCGCCACTACTAGTCCGCGCAGTCCAGAGGGCTC 301
 OY 345 TCAAGACCGCGCTGAGAGGGCTCGCGGGGCTCGACGGGAAACCTGTTGAGCATGACC 404
 DB 302 TCAAGACCGCGCTGAGAGGGCTCGCGGGGCTCGACGGGAAACCTGTTGAGCATGACC 361
 OY 405 AGAGCAAGAAAGATATGATGATCATGACCTTTGCTGACACAGACCTCTCCAGATCAACC 464
 DB 362 AGAGCAAGAAAGATATGATGATCATGACCTTTGCTGACACAGACCTCTCCAGATCAACC 421
 OY 465 AGACCCGGCTGAGATTCACCTTCTGCTGATAGTGGCAGTGGCATGAGAGTCCGCGAGA 524
 DB 422 AGACCCGGCTGAGATTCACCTTCTGCTGATAGTGGCAGTGGCATGAGAGTCCGCGAGA 481
 OY 525 CCGGCTTCATGTTCTTGTGCGAGTTCGCCCAATGCGCAGACCATGAAATTAAGAG 584
 DB 482 CCGGCTTCATGTTCTTGTGCGAGTTCGCCCAATGCGCAGACCATGAAATTAAGAG 541
 OY 585 TTCTTGTCTAAGACCATATGACACAA-CCTCACCTTGAAGAGTACGTGTTGCA 642
 DB 542 TTCTTGTCTAAGACCATATGACACAAACCTTGAAGAGTACGTGTTGCA 601
 OY 643 GGTGATGCGCATGCTGCTGATGACCTTCTCTGAGAGCTGAACTCAAGTCTGTCAG 702
 DB 602 GGTGATGCGCATGCTGCTGATGACCTTCTCTGAGAGCTGAACTCAAGTCTGTCAG 660
 OY 703 CCAGGAGACCTTACTCTGAGCTGTACAGAAAGCCAGTGGCCACAGTCTTCTGAT 762
 DB 661 CCAGGAGACCTTACTCTGAGCTGTACAGAAAGCCAGTGGCCACAGTCTTCTGAT 720
 OY 763 CCGGCTGCTTTTCCACAGGCTTTTGTGGCAGCCAGGTAAGGTTGAGGCGCAAGCA 822
 DB 721 CCGGCTGCTTTTCCACAGGCTTTTGTGGCAGCCAGGTAAGGTTGAGGCGCAAGCA-CC 778
 OY 823 TCGGCTTCCCGCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 856
 DB 779 TCGGCTTCCCGCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 812

RESULT 7
LOCUS BF232704 816 bp mRNA linear EST 14-NOV-2000
DEFINITION 602023292F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:4158766 5',
mRNA sequence.
ACCESSION BF232704
VERSION BF232704.1 GI:11142342
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 816)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@pds-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L19M9435 row: 9 column: 23
High quality sequence stop: 714.
Location/Qualifiers
1..816
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4158766"
/clone_1lb="NCI_CGAP_L19"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: Liver; Vector: PCMV-SPORE6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 167 a 253 c 221 g 175 t
ORIGIN
Query Match 42.0%; Score 653.8; DB 10; Length 816;
Best Local Similarity 97.5%; Pred. No. 1.8e-171;
Matches 738; Conservative 0; Mismatches 12; Indels 7; Gaps 7;
QY 26 GTCACATCTCTCCAGAGGTCCTGTCGCCAGACAGAGTTGAG-CAGTCCCGTTGAGA 84
DB 1 GTCACATCTCTCCCA-GGTCCTGTCGCCAGACAGAGTTGAGAGCCACTCCGTTGAGA 59
QY 85 CCTGATATAGAGCTTGGTCTTAAAGAGGCTATCCGCCAGATGGCCCTCCCTT 144
DB 60 CCTGATATAGAGCTTGGTCTTAAAGAGGCTATCCGCCAGATGGCCCTCCCTT 118
QY 145 GCTCTGCTCTTCT 204
DB 119 GCTCTGCT 178
QY 205 ATGCCCAAGCATTTGGGGGTCCTCTTGAAGGAGAGGAGCCGAGAGCTCTCTCTGA 264
DB 179 ATGCCCAAGCATTTGGGGGTCCTCTTGAAGGAGAGGAGCCGAGAGCTCTCTCTGA 238
QY 265 TTGGGCAAGAAAGATATCTGACAGAGCTGACCGCCAGCCGCCCATCTACTGTCG 324
DB 239 TTGGGCAAGAAAGATATCTGACAGAGCTGACCGCCAGCCGCCCATCTACTGTCG 298
QY 325 GCCAGTGTCCAGAGGGGCTCTCAAGACCGGCTGACGCCCTCCGGGGGCTCTGACAGGCA 384
DB 299 GCCAGTGTCCAGAGGGGCTCTCAAGACCGGCTGACGCCCTCCGGGGGCTCTGACAGGCA 358
QY 385 AACCTGTGGAGCATGACACAGACAGCAAGAAATATGATCATCAGCTTTGCTACAC 444

DB 359 AACCTGTGGAGCATGACACAGACAGCAAGAAATATGATCATCAGCTTTGCTACAC 418
QY 445 AGACTCTTCACAGCATCAACACAGACCGGCTCGAGTTCCACTTCTCTGTAGATGGCCAG 504
DB 419 AGACTCTTCACAGCATCAACACAGACCGGCTCGAGTTCCACTTCTCTGTAGATGGCCAG 478
QY 505 TGGCATGAGAGGTCGGGACAGACCGGCTTCAGTTCCTTCGTGACAGTTCCGCCAATGGCCAC 564
DB 479 TGGCATGAGAGGTCGGGACAGACCGGCTTCAGTTCCTTCGTGACAGTTCCGCCAATGGCCAC 538
QY 565 CCAGACCATGAATATATAGAGTTCTTGTGCTAAGACCATATGACACCAACCTGACCTGAC 624
DB 539 CCAGACCATGAATATATAGAGTTCTTGTGCTAAGACCATATGACACCAACCTGACCTGAC 598
QY 625 AAGTCATGACGTGTGTCAGAGTGATGCCAGGTGCTGATACCAAGCTTCTCTGGACCTGA 684
DB 599 CAGTCAGTACGTGTGTCAGAGTGATGCCAGGTGCTGATACCAAGCTTCTCTGGACCTGA 658
QY 685 AGC-TCAGCTGCTTGA-GCCAGGACACCTTAC-TCGGAGCTGTGTCAGGAAGGCA 741
DB 659 AGCTTAAGCTTTTGCAGGCGCAGGACACTTACTTGTGAGCTGTGATCCGAAAGCC- 717
QY 742 GGTGGCCACAGTTCCTGATCCTGGGCTGTTTCC 778
DB 718 CGTGGCCACAGTTCCTGATCCTGGGCTGTTTCC 754
RESULT 8
LOCUS BF533968 975 bp mRNA linear EST 11-DEC-2000
DEFINITION 602075129F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:4212175 5',
mRNA sequence.
ACCESSION BF533968
VERSION BF533968.1 GI:11621331
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 975)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE Unpublished (1999)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@pds-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L19M9782 row: 1 column: 08
High quality sequence stop: 659.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:4212175"
/clone_1lb="NCI_CGAP_L19"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: Liver; Vector: PCMV-SPORE6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 190 a 297 c 266 g 222 t
ORIGIN
Query Match 41.3%; Score 643.6; DB 10; Length 975;
Best Local Similarity 97.2%; Pred. No. 1.4e-168;
Matches 698; Conservative 0; Mismatches 14; Indels 6; Gaps 4;

97 GCTTGGGCTTTAAGAGGCTATCTCCAGCAATGGCCCTCTGCTGGCTCT 156
 1 GCTTGGGCTTTAAGAGGCTATCTCCAGCAATGGCCCTCTGCTGGCTCT 60
 157 TCTGTTCTGACTCCACACAGTATGTAACCCCAAACTGAGGGTCCATGCCAGCATG 216
 61 TCTGTTCTGACTCCACACAGTATGTAACCCCAAACTGAGGGTCCATGCCAGCATG 120
 217 TTGGGGTGGCTATCTTTGACCTGGAGAGCCAGGGAGTGTCTTCTGCTTTGGCCAGAA 276
 121 TTGGGGTGGCTATCTTTGACCTGGAGAGCCAGGGAGTGTCTTCTGCTTTGGCCAGAA 180
 277 AAGTATCCGGAGCAAG-CTGCACCTCAGCAGAGCCGCCCTACTACTAGTGGCCAGTGTCCA 335
 181 AAGTATCTCTGGAGCAAGTGTGCACTCAGCAGAGCCGCCCTACTACTAGTGGCCAGTGTCCA 240
 336 GAGGGCTCTCAAGACCCGCTGAGAGCCGCTCCGCGGCTCCAGAGGAAACCTGTTTG 395
 241 GAGGGCTCTCAAGACCCGCTGAGAGCCGCTCCGCGGCTCCAGAGGAAACCTGTTTG 300
 396 AGCATACCAAGAGCAAGAAATATGATATCATGCTTTGGTGCACACAGCTCTTCCA 455
 301 AGCATACCAAGAGCAAGAAATATGATATCATGCTTTGGTGCACACAGCTCTTCCA 360
 456 GCATCAACCAAGACCCGCTGAGAGCCGCTCCGCGGCTCCAGAGGAAACCTGTTTG 515
 361 GCATCAACCAAGACCCGCTGAGAGCCGCTCCGCGGCTCCAGAGGAAACCTGTTTG 420
 516 TCCGCGAGACCCGCTCATGTTCTGCTGAGTGTCCGCGGCTCCAGAGGAAACCTGTTTG 575
 421 TCCGCGAGACCCGCTCATGTTCTGCTGAGTGTCCGCGGCTCCAGAGGAAACCTGTTTG 480
 576 ATTTAAGAGTCTTGTGCTGAGAGCAATATGATATCATGCTTTGGTGCACACAGCTCTTCCA 635
 481 ATTTAAGAGTCTTGTGCTGAGAGCAATATGATATCATGCTTTGGTGCACACAGCTCTTCCA 540
 636 TGTGAGAGTGTGCTGAGAGCAATATGATATCATGCTTTGGTGCACACAGCTCTTCCA 694
 541 TGTGAGAGTGTGCTGAGAGCAATATGATATCATGCTTTGGTGCACACAGCTCTTCCA 600
 695 GCTTGCACAGCAGGAGCACTTACTCTGAGAGCTGTACAGAAAGCCAGTGGCCACAGT 754
 601 GCTTGCACAGCAGGAGCACTTACTCTGAGAGCTGTACAGAAAGCCAGTGGCCACAGT 658
 755 TCTGATCTGAGGCTGTGTTTCCACAGGCC--TTTGTGAGAGCCAGTAAAGGT 810
 659 TCTGATCTGAGGCTGTGTTTCCACAGGCCCTTTTGTGAGCCAGTAAAGGT 716

RESULT 9 636 bp mRNA linear EST 14-NOV-2000
 LOCUS BF236906
 DEFINITION 602026526P1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:4161721, 5',
 mRNA sequence.
 ACCESSION BF236906
 VERSION BF236906.1 GI:1150823
 KEYWORDS EST.
 SOURCE house mouse
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 636)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-femail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: L1AM9443 row: c column: 08
 High quality sequence stop: 634.
 Location/Qualifiers
 1. 636
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4161727"
 /clone_lib="NCI_CGAP_L19"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: liver; Vector: pCMV-Sport6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: 01190 df.
 Average insert size 1.9 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 144 a 189 c 167 g 136 t
 ORIGIN

Query Match 32.7%; Score 509; DB 10; Length 636;
 Best Local Similarity 96.7%; Pred. No. 4,4e-131;
 Matches 616; Conservative 0; Mismatches 10; Indels 11; Gaps 9;

49 GGTGCCCCAGACAGAGTTTAAAG-CACTCCCGTTGAGACCCCTGAATATAGCTTTGGCTCC 107
 1 GGTGCCCCAGACAGAGTTTAAAGCACTCCCGTTGAGACCCCTGAATATAGGCTTTGGCTCC 59
 108 TTTAAGAGGCTATCTCTCCAGCAATGGCCCTCTGCTGCTCT--GGCTCTTGTCTCTG 166
 60 TTTAAGAGGCTATCTCTCCAGCAATGGCCCTCTGCTGCTCTGCTGCTCTGCTCTGCTG 119
 167 ACTCAACCAAGTATGTAAGACCCCAAACTGAGGGTCCATGCCAGCATGTTGGGCTCC 226
 120 ACTCAACCAAGTATGTAAGACCCCAAACTGAGGGTCCATGCCAGCATGTTGGGCTCC 179
 227 ATCTTGAAGCTGAGAGCCAGGGGAGCTGCTTCGATTTGGCCAA--GAAAAGTATC 283
 180 ATCTTGAAGCTGAGAGCCAGGGGAGCTGCTTCGATTTGGCCAAAGTATGATC 239
 284 CTGAGACAA-CTTGCACCTCA-GCCAGCCGCCCATACTAGTGGCCAGTGTG-CAGAGG 340
 240 CTGAGACAACTGCTCAGCTCATATGCGACGCGCCCATACTAGTGGCCAGTGTGCGAGAGG 299
 341 GCTCTCAAGCCCGCTGCAAGCGCTCCGCGGCTCTGAGAGGAAACCTGTGTGAGCAT 400
 300 GCTCTCAAGCCCGCTGCAAGCGCTCCGCGGCTCTGAGAGGAAACCTGTGTGAGCAT 359
 401 GACGAGACAAAGATATGATCATCAGTTTGTGAGACAGAGCTCTCCAGCATC 460
 360 GACGAGACAAAGATATGATCATCAGTTTGTGAGACAGAGCTCTCCAGCATC 419
 461 AACGAGACCCGCTGAGATTCACCTTCTGTGATGATGAGCCAGTGGAGTCCGG 520
 420 AACGAGACCCGCTGAGATTCACCTTCTGTGATGATGAGCCAGTGGAGTCCGG 479
 521 CAGACCCGCTCATGTTCTTCTGAGAGTCCGCGGCTCTGAGAGCAAGCCAGCAACA-CTAATAT 579
 480 CAGACCCGCTCATGTTCTTCTGAGAGTCCGCGGCTCTGAGAGCAAGCCAGCAACAATAT 539
 580 AAGAGTCTTGTGATGAGCAATATGAG-ACCAACTCACTTGAACATGCTAGTACGTGG 638
 540 AAGAGTCTTGTGATGAGCAATATGAGCAACTCACTTGAACATGCTAGTACGTGG 599
 639 TGCAGTGAATGCCAGTGTGCTGATCCAGCTTCTCT 675
 600 TGCAGTGAATGCCAGTGTGCTGATCCAGCTTCTCT 636

RESULT 10 1011 bp mRNA linear HTC 22-JAN-2002
 LOCUS BC020693
 DEFINITION Homo sapiens, similar to Inhibin, beta C, clone IMAGE:4723762,
 mRNA.

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 22:15:33 ; Search time 41 Seconds
(without alignments)

953,609 Million cell updates/sec

Title: US-09-684-383-4

Perfect score: 1850
Sequence: 1 MASSLLALLFLPTTVNP.....DSNIKTDIPDWEACGCS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1844	99.7	352	19	AAW60617
2	1398	75.6	352	17	AAR89729
3	1387	75.0	352	22	AAB70530
4	594	32.1	350	17	AAR92754
5	594	32.1	350	22	AAW93672
6	585	31.6	350	19	AAW60619
7	581.5	31.4	350	19	AAW60618
8	550.5	29.8	427	8	AAW70200
9	548.5	29.6	407	21	AAW92017
10	548.5	29.6	407	21	AAW92019
11	543	29.4	353	8	AAW70204

12	540	29.2	426	8	AAW70203	Sequence of human
13	540	29.2	426	21	AAW92016	Human inhibin A be
14	540	29.2	426	21	AAW92018	Human activin A su
15	538	29.1	426	11	AAR05413	BUF-3 human differ
16	531	28.7	351	8	AAW70201	Sequence of porcin
17	450	28.3	127	12	AAR10991	Xenopus Bone Morph
18	444	24.0	87	14	AAR45447	TGF-beta-like clon
19	440.5	23.8	303	22	AAU02908	Sequence of bovine
20	431	23.3	288	7	AAW60518	Inhibin betaB C-t
21	401.5	21.7	121	22	AAW73203	Inhibin betaA C-t
22	398	21.5	122	22	AAW73202	Sequence of human
23	396	21.4	130	7	AAW60520	Activin-like pepti
24	374.5	20.2	115	13	AAR26482	Activin-like pepti
25	374	20.2	116	13	AAR26481	Human KIM-5M. Hom
26	373.5	20.2	115	13	AAR25129	Human KIM-5M. Hom
27	373.5	20.2	115	14	AAR31623	BUF-4. Synthetic.
28	373.5	20.2	115	13	AAR25127	Activin B. Synthet
29	372	20.1	130	12	AAR10990	Xenopus Bone Morph
30	371	20.1	116	8	AAW71196	Sequence of verteb
31	371	20.1	116	8	AAW71176	Second protein cha
32	371	20.1	116	9	AAW80019	Sequence of the 14
33	371	20.1	116	9	AAW82061	Polypeptide BUF-3
34	371	20.1	116	11	AAR05443	Monomer A of BUF-4
35	371	20.1	116	11	AAR08215	Follicle stimulat
36	371	20.1	116	13	AAR25128	Activin AB. Synth
37	371	20.1	116	14	AAR31622	BUF-3. Synthetic.
38	371	20.1	116	21	AAW67949	Human activin A SE
39	368.5	19.9	115	8	AAW71197	Sequence of verteb
40	368.5	19.9	115	8	AAW71177	Second protein cha
41	368.5	19.9	115	11	AAR08216	Follicle stimulat
42	368	19.9	116	12	AAR12088	16.5 kD subunit of
43	363.5	19.6	115	9	AAW80020	Sequence of the 14
44	363	19.6	116	11	AAR05444	Monomer B of BUF-4
45	359	19.4	116	9	AAR81906	N-terminal of Inhl

ALIGNMENTS

RESULT 1	AAW60617	standard. Protein: 352 AA.
ID	AAW60617	
XX	AAW60617	
AC	AAW60617	
XX	AAW60617	
DT	01-FEB-1999	(first entry)
XX	01-FEB-1999	
DE	Murine liver activin beta c polypeptide.	
XX	Murine liver activin beta c polypeptide.	
KW	Liver activin: beta c; beta e; cell differentiation; haematopoiesis;	
KW	erythroid; ovarian follicular maturation; hormone; neuronal survival;	
KW	spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;	
KW	osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunosup;	
KW	menstrual disorder; transgenic; modulator.	
OS	Mus sp.	
XX	Mus sp.	
XX	Mus sp.	
FT	Key	Location/Qualifiers
FT	Peptide	1..20
FT	Modified-site	/note="signal sequence"
FT	Modified-site	111..113
FT	Modified-site	/note="Asn is putatively N-glycosylated"
FT	Modified-site	143..145
FT	Modified-site	/note="Asn is putatively N-glycosylated"
FT	Modified-site	161..163
FT	Modified-site	/note="Asn is putatively N-glycosylated"
FT	Modified-site	173..175
FT	Modified-site	/note="Asn is putatively N-glycosylated"
FT	Domain	21..236
FT	Domain	/note="propeptide domain"
FT	Cleavage-site	230..236
FT	Cleavage-site	/note="endoproteolytic cleavage site"
FT	Domain	237..352


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DB 120 SDRTAGDREYQASLMFVQLEPSNTWTIKRVVLVGLGHNTNLATQYLEVDASGMHQ 179
OY 180 LLLGPEAQAACSGHILTELVPEAOVHSSLLIGWFSRRPVAOVRECKHRRRGID 239
DB 180 LPLGPEAQAACSGHILTELVPEAOVHSSLLIGWFSRRPVAOVRECKHRRRGID 239
OY 240 CGGSRMCCROEFVDFREIGWMDWIIOPEGYAMNFCIGCCPLHAGMPGIAASFHTAVL 299
DB 240 CGGSRMCCROEFVDFREIGWMDWIIOPEGYAMNFCIGCCPLHAGMPGIAASFHTAVL 299
OY 300 NLKANAAGTGRGSCCPTSRRLSLLYDRDSNIVKTDIPDMVAVGCGS 352
DB 300 NLKANAAGTGRGSCCPTSRRLSLLYDRDSNIVKTDIPDMVAVGCGS 352

RESULT 3
AAB70530 standard; Protein: 352 AA.
XX
AC AAB70530;
XX
DT 08-MAY-2001 (first entry)
XX
DE Human TGF-beta MP121 protein sequence SEQ ID NO:4.
XX
XX Human: transforming growth factor-beta; monomeric protein; MP52;
XX MP121; dimeric protein; TGF-beta; vulnery; antilicer; neutrophic;
XX neuroprotective; antiliferility; osteopathic; gene therapy; bone;
XX cartilage; dental; wound healing; connective tissue.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT MISC-difference 316
FT /note="unspecified"
XX
PN EP1074620-A1.
XX
PD 07-FEB-2001.
XX
PF 06-AUG-1999; 99EP-0115613.
XX
PR 06-AUG-1999; 99EP-0115613.
XX
XX (HUGE-) HYGENE AG C/O MAEDER & BAUMGARTNER TREUH.
XX
PA WPI: 2001-228100/24.
XX
DR N-PSDB; AAF74421.
XX
XX
XX Novel monomeric protein of transforming growth factor-beta family for
XX prevention or therapy of diseases associated with bone, cartilage
XX damage, promotion of wound healing, has substitution or deletion of
XX cysteine.
XX
XX Claim 10; Page 21-22; 31pp; English.
XX
XX The present invention describes a protein (I) selected from the members
XX of the transforming growth factor-beta (TGF-beta) superfamily, which is
XX monomeric due to substitution or deletion of a cysteine which is
XX responsible for dimer formation. Also described are: (1) nucleic acid
XX (II) encoding (1); (2) expression vector (III) containing (II) in a
XX suitable vector system; (3) host cell (IV) containing (III) capable of
XX producing (I); and (4) a pharmaceutical composition (V) containing (I),
XX (II), (III) or (IV). (1) has vulnery, antilicer, neutrophic,
XX neuroprotective, antiliferility and osteopathic activities, and can be
XX used in gene therapy. (V) is useful for the prevention or therapy of
XX diseases for which also the dimeric form of the protein would be
XX indicated. Diseases treatable include bone and/or cartilage disease or
XX and/or cartilage damage or affecting bone and/or cartilage disease or
XX situations in which cartilage and/or bone growth is desirable, for spinal
XX fusion, for damaged or diseased tissue associated with connective tissue
XX including tendon and/or ligament, periodontal or dental tissue including

```

```

CC dental implants, neural tissue including CNS tissue and neuropathological
CC situations, tissue of the sensory system, liver, pancreas, cardiac,
CC blood vessel, renal, uterine and thyroid tissue, skin, mucous membrane,
CC endothelium, epithelium, for promotion or induction of nerve growth,
CC tissue regeneration, angiogenesis, wound healing including ulcers, burns,
CC injuries or skin grafts, induction of proliferation of progenitor cells
CC or bone marrow cells, for maintenance of a state of proliferation or
CC differentiation, for treatment or preservation of tissue or cells for
CC organ or tissue transplantation, for integrity of gastrointestinal lining
CC and for treatment of disturbances in fertility, contraception or
CC pregnancy. The present sequence represents the specifically claimed
CC TGF-beta monomeric protein MP121, from the present invention.
CC
XX
SQ Sequence 352 AA:
XX
XX Query Match 75.0%; Score 1387; DB 22; Length 352;
XX Best Local Similarity 75.9%; Pred. No. 3.1e-125;
XX Matches 268; Conservative 32; Mismatches 51; Indels 2; Gaps 2;
XX
OY 1 MASSLLALFLTPPTVVPKTEGCPACMGAFIDLESORELLDLAKSLDLKHLHSQR 60
DB 1 MTSSLLALFLLPPTVATPRAGGCGPTELESORELLDLAKSLDLKHLHSQR 60
OY 61 PILSPVSGALKALQRLGPRRETLERHQRQREYELISPAVDLSINOTLREHFS 120
DB 61 PTLNRPVSRALRTALQHLHGVPGALIE-DNRQECILISPAETGLSTINOTLREHFS 119
OY 121 G-RMASEMEYRQTRFMPFVQFPHNATOTNIRVLYLRPYDTLTLTSGYVAVNASCYQ 179
DB 120 SDRTAGDREYQASLMFVQLEPSNTWTIKRVVLVGLGHNTNLATQYLEVDASGMHQ 179
OY 180 LLLGPEAQAACSGHILTELVPEAOVHSSLLIGWFSRRPVAOVRECKHRRRGID 239
DB 180 LPLGPEAQAACSGHILTELVPEAOVHSSLLIGWFSRRPVAOVRECKHRRRGID 239
OY 240 CGGSRMCCROEFVDFREIGWMDWIIOPEGYAMNFCIGCCPLHAGMPGIAASFHTAVL 299
DB 240 CGGSRMCCROEFVDFREIGWMDWIIOPEGYAMNFCIGCCPLHAGMPGIAASFHTAVL 299
OY 300 NLKANAAGTGRGSCCPTSRRLSLLYDRDSNIVKTDIPDMVAVGCGS 352
DB 300 NLKANAAGTGRGSCCPTSRRLSLLYDRDSNIVKTDIPDMVAVGCGS 352

RESULT 4
AAR92754 standard; Protein: 350 AA.
XX
AC AAR92754;
XX
DT 21-JUL-1996 (first entry)
XX
DE Human growth differentiation factor-12.
XX
XX Growth differentiation factor-12; GDF-12; liver; cell proliferation;
XX cancer; diagnosis; therapy; transforming growth factor beta.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 198..200
FT /label= N-glycosylation-site
FT Cleavage-site 232..236
FT /label= C-terminal-region
FT Region 237..350
FT /label= C-terminal-region
FT /note= "GPR-12 active C-terminal fragment"
XX
XX W09602559-A1.
XX
XX 01-FEB-1996.
XX
XX 12-JUL-1995; 95WO-US08745.
XX

```

PR 26-SEP-1994: 94US-0311370.
 PR 13-JUL-1994: 94US-0274215.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.
 PA
 PI Esquelea AF, Lee S;
 XX
 XX WPI: 1996-105850/11.
 DR N-PSDB: AAT16883.
 XX
 PT DNA encoding Growth Differentiation Factor-12 - used in diagnostic
 PT and therapeutic methods esp. in methods for treating a cell
 PT proliferative disorder of liver origin
 XX
 PS Claim 3: Page 40-43; 52pp; English.
 XX
 CC Human growth differentiation factor-12 (GDF-12 - AAR92754) is a new
 CC member of the transforming growth factor beta superfamily that is
 CC expressed specifically in liver. It can be obtained by expression
 CC of a cDNA clone (AAT16883) derived from adult liver in transformed
 CC host cells. GDF-12 possesses activities that will make it useful
 CC in the treatment of liver disorders, e.g. disease states in which
 CC liver function is compromised, or cellular proliferative disorders
 CC such as hepatocellular carcinoma. It can also be used to expand
 CC liver cells in culture and to raise diagnostic antibodies.
 CC
 SO Sequence 350 AA:
 Query Match 32.1%; Score 594; DB 17; Length 350;
 Best Local Similarity 39.3%; Pred. No. 8.2e-49;
 Matches 141; Conservative 51; Mismatches 109; Indels 58; Gaps 11;
 OY 22 TGGCPACMGATFLEESORELLDLAKKSITDKLHSORPLSRPVSGALKTALQRLR- 80
 DB 22 TGSVCPSGSGSKLAPQAEALVLELAKQQLDGLHLSRPRTIHPPOALTRALRLQRP 81
 OY 81 ---GPRRRETLLEHQROEYEIISPAD-TDLSSINQRLIEFHSGMAAGMEVROTRFMF 136
 DB 82 GSVAPNGE-----EVLSPATVDTSTAYSLSLTFHLS--TPRSHNLHYARLML 128
 OY 137 FVQFPNATOTMTN-----RVLVLRPYDTNLTLSQYVVYVNASGMYQLLGP 184
 DB 129 HVLPTLPCTLCRIFRMGPRRRRSGSRLLAEHNTNL-----GMHTLTLP 175
 OY 185 EAQAACSGGLTLEIVPESOVAHSSL-----ILGFSSH-RPVVAQVRVE--GKHRYRR 235
 DB 176 SGLRGEKSGVLKIQDLDRPLEGNTVTGQPRRLDTAGHQDPLEIKIRANEPGAGARRR 235
 OY 236 RGIDCGGSRMCRQEFVDFREIGNMDWIIQEGYAMNFCGQCPPLVAVAGPGISASFH 295
 DB 236 RTPTCEPATPLCCRRDHYVDFQELGMDWIIQPEGYQLANSCGQCPPLHAGSPGIAASFH 295
 OY 296 TAVNLTKANA--AAGTTGSGCCVPTSRRLSLLYDRDSNIIVKTDIDMNVVEACGCS 352
 DB 296 SAVFSLLKANPMPAST-----SCCVPTARRPLSLLYLDHNGNVVKTVDPMVVEACGCS 350
 RESULT 5
 AAM93672
 ID AAM93672 standard; Protein: 350 AA.
 XX
 AC AAM93672;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide, SEQ ID NO: 3558.
 XX
 KM Human; full length cDNA; cDNA synthesis; oligo-capping.
 OS Homo sapiens.
 XX
 PN EPI130094-A2.
 XX

PD 05-SEP-2001.
 XX
 PF 07-JUL-2000; 2000EP-0114089.
 XX
 PR 08-JUL-1999: 99JP-0194486.
 PR 11-JAN-2000; 2000JP-0118774.
 PR 02-MAY-2000; 2000JP-0183765.
 XX
 XX
 PA (HELI-) HELIX RES INST.
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 DR WPI: 2001-524255/58.
 DR N-PSDB: AAK94607.
 XX
 PT 830 Primers useful for synthesizing full length cDNA clones and their
 PT use in genetic manipulation -
 XX
 PS Claim 8: SEQ ID NO 3558; 1380pp + sequence listing; English.
 XX
 CC The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been
 CC isolated and nucleotide sequences of 5' and 3' ends of the cDNA
 CC molecules have been determined. Primers for synthesizing the full length
 CC cDNA are useful for clarifying the function of the protein encoded by
 CC the cDNA. The full length clones were obtained by construction of full
 CC length enriched cDNA libraries that were synthesized by the oligo-capping
 CC method. The primers enable the production of the full length cDNA easily
 CC without any special methods. The present sequence is a polypeptide
 CC encoded by a full length human cDNA of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in CD-ROM format directly from EPO.
 CC
 SO Sequence 350 AA:
 Query Match 32.1%; Score 594; DB 22; Length 350;
 Best Local Similarity 39.3%; Pred. No. 8.2e-49;
 Matches 141; Conservative 51; Mismatches 109; Indels 58; Gaps 11;
 OY 22 TGGCPACMGATFLEESORELLDLAKKSITDKLHSORPLSRPVSGALKTALQRLR- 80
 DB 22 TGSVCPSGSGSKLAPQAEALVLELAKQQLDGLHLSRPRTIHPPOALTRALRLQRP 81
 OY 81 ---GPRRRETLLEHQROEYEIISPAD-TDLSSINQRLIEFHSGMAAGMEVROTRFMF 136
 DB 82 GSVAPNGE-----EVLSPATVDTSTAYSLSLTFHLS--TPRSHNLHYARLML 128
 OY 137 FVQFPNATOTMTN-----RVLVLRPYDTNLTLSQYVVYVNASGMYQLLGP 184
 DB 129 HVLPTLPCTLCRIFRMGPRRRRSGSRLLAEHNTNL-----GMHTLTLP 175
 OY 185 EAQAACSGGLTLEIVPESOVAHSSL-----ILGFSSH-RPVVAQVRVE--GKHRYRR 235
 DB 176 SGLRGEKSGVLKIQDLDRPLEGNTVTGQPRRLDTAGHQDPLEIKIRANEPGAGARRR 235
 OY 236 RGIDCGGSRMCRQEFVDFREIGNMDWIIQEGYAMNFCGQCPPLVAVAGPGISASFH 295
 DB 236 RTPTCEPATPLCCRRDHYVDFQELGMDWIIQPEGYQLANSCGQCPPLHAGSPGIAASFH 295
 OY 296 TAVNLTKANA--AAGTTGSGCCVPTSRRLSLLYDRDSNIIVKTDIDMNVVEACGCS 352
 DB 296 SAVFSLLKANPMPAST-----SCCVPTARRPLSLLYLDHNGNVVKTVDPMVVEACGCS 350
 RESULT 6
 AAM60619
 ID AAM60619 standard; Protein: 350 AA.
 XX
 AC AAM60619;
 XX
 DT 01-FEB-1999 (first entry)
 XX

Query	22	TEGPCACWGIATFDESGRELLDLAKKSTILDKRTHLQRPILSRHVSRCALKTALQRIK	80
Matches	139	Conservative 53; Mismatches 109; Indels 58; Gaps 11	
Best Local Similarity	38.7%	Pred. No. 6,1e-48;	
Score	585	DB 19; Length 350;	
Sequence	350 AA;		
Query Match	31.68;	Score 585; DB 19; Length 350;	
Best Local Similarity	38.7%	Pred. No. 6,1e-48;	
Matches	139	Conservative 53; Mismatches 109; Indels 58; Gaps 11	

Accession	Protein	Length	Weight	PI	Source	Species	Notes
22	TGSCVPCGGCKSLAQRNALVLELAKQVILEGHLILTSRPRITNPPQAAVTRALRLRLOP	81	9.1	5.1	Human	Testis	
QY	81 ---GPRRETLLEHQROEEYEIISFAD-TDLSSTINQTRLEFHSFGMASGMEYRQTRFME	136	14.5	5.1	Human	Testis	
Db	82 GSVAPNGNE-----EVISFAVTVDTSTAYSSSLTFHLIS--TPRSHILYHARLM	128	14.5	5.1	Human	Testis	
QY	137 FVQPRHNATQTMNI-----RVLLRPRVDNLTLTSQVYVYVQVNASGMYQLLGP	184	20.5	5.1	Human	Testis	
Db	129 HVLPRLEPDLCLRLFMRGPRRRRGGSTLLAEHNIITNL-----GWHTLTLP	175	19.5	5.1	Human	Testis	
QY	185 EAQAACSGGHLTLELVPSQVAAHSSL-----ILGWFSH-RPPVAAOVRYE--GKIRIVR	235	26.5	5.1	Human	Testis	
Db	176 SGLRGEKSGVLKLDIDCRPLENGNSTVTGQPRRLIDDTGAHQOPELEKIRANEPGAGRARR	235	26.5	5.1	Human	Testis	
QY	236 RGIIDGGSGRWKCGQEEFVDFREIRGMNDMIIOPEGVAMNCTGGCPPLHVGMPGISASFH	295	33.5	5.1	Human	Testis	
Db	236 RPTPEPATPLCCRRDHDVDFQELGMRDMLIOPGYQLNCTGSGCCPPLHVGMPGISASFH	295	33.5	5.1	Human	Testis	
QY	296 TAVLLMLLKANA--AAGTTGSGSCCVPTSRPLSLYYDRDSNIYKTDIPDMVVEAGCS	352	39.5	5.1	Human	Testis	
Db	296 SAVFSLILKANNPWRASST---SCCPTPARRPLSLYLDHNGNMYKTDVPMVVEAGCS	350	39.5	5.1	Human	Testis	
RESULT 7							
AAW60618	AAW60618 standard; Protein; 350 AA.						
XX	AAW60618:						
AC	01-FEB-1999 (first entry)						
XX							
DE	Murine liver activin beta e polypeptide.						
XX							
KW	Liver activin: beta c; beta e; cell differentiation; hematopoiesis; erythroid; ovarian follicular maturation; hormone; neuronal survival; spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis; osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunosensitivity; menstrual disorder; transgenic; modulator.						
XX							
OS	Mus sp.						
XX							
FT	Key	Location/Qualifiers					
FT	Peptide	1..21					
FT		/note="signal sequence"					
FT	Domain	22..236					
FT		/note="propeptide domain"					
FT	Modified-site	198..200					
FT		/note="Asn is putatively N-glycosylated"					
FT	Cleavage-site	232..236					
FT		/note="endoproteolytic cleavage site"					
FT	Domain	237..349					
FT		/note="mature growth factor domain"					
XX							
PN	MO9822492-A1.						
XX							
PD	28-MAY-1998.						
XX							
PF	20-NOV-1997; 97MO-US20882.						
XX							
PR	20-NOV-1996; 96US-0752919.						
XX							
PA	(UNMI) UNIV MICHIGAN.						
XX							
PI	Bonadio J, Fang J;						
XX							
DR	WPI; 1998-312408/27.						
XX	N-PDB; AAV38238.						
PT	New isolated nucleic acid encoding sub-units of liver activin						
PT	useful for regulating growth and differentiation of cells, e.g. for						
PT	treating liver, bone and haematopoietic disorders						
XX							
PS	Claim 16; Fig 2; 141pp; English.						

XX This represents a murine liver activin beta e polypeptide. Sequences
 CC derived from a beta c cDNA clone is used for screening and cloning the
 CC activin beta e gene. Disorders of cell growth or differentiation (or
 CC susceptibility to them) are diagnosed by measuring liver activin gene
 CC activity or by detecting a mutation in the liver activin gene. Disorders
 CC of haemopoiesis, erythroid differentiation, ovarian follicular
 CC maturation, hormone secretion, neuronal survival, spermatogenesis, bone
 CC formation, insulin secretion or cardiac morphogenesis are some conditions
 CC that can be diagnosed using the liver activin. Cell growth and
 CC differentiation can be stimulated by treatment with an liver activin
 CC compound or agent that upregulates the compound's expression. Antagonists
 CC can be used to treat liver diseases while agonists can be used to
 CC increase growth and regeneration of liver tissue. The liver activin
 CC compound may also induce bone growth (e.g. for treating osteoporosis or
 CC osteomalacia) or haemopoiesis, particularly erythropoiesis, e.g. for
 CC treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies
 CC are useful in immunosays, to generate anti-idiotypic antibodies (which
 CC bind to liver activin receptors) and to inhibit liver activin. Also,
 CC transgenic animals containing liver activin gene can be used to produce
 CC the liver activin (in correctly processed and modified forms) proteins,
 CC or the transgenic animals, are useful for screening for liver activin
 CC modulators.

SQ Sequence 350 AA:

Query Match 31.44; Score 581.5; DB 19; Length 350;

Best Local Similarity 37.74; Pred. No. 1.3e-47;

Matches 140; Conservative 66; Mismatches 110; Indels 55; Gaps 14;

OY 5 LLLALFLPTTVVNPRTGCPACWGAIFDLESORELLDLAKKSILDKLSORPLIS 64
 DB 12 LLMALWV-----QSRKSCPCGCGPTLAPQGERALVLELAKQQLLEGILTSRRPRT 64
 OY 65 RPYSGALKTLQRLKGR-----RETLLEHDOKEVEEIIISPAD-TDLSSINOTRE 116
 DB 65 RPLPMAALTRALRLQ-PRKSWPGNRE-----KVISFATIIDKSTSTYRSMLT 111
 OY 117 FHFSGRMASGMEVOTRMPFVOPRNATOTMIRIVLVLPYOTNL---TTSQYVVOV 172
 DB 112 FOLSLMNHNL-----YHARLMLHVPSPFGTLYLR-IFRCGTTGRGRTFLAEN-OT 163
 OY 173 NASGWYOLLGPEAQAACSGHLLTEL-----VPESQVHNSLIIGWF-SHHPFAAOV 225
 DB 164 TSSGMHPLTPSSGLRSEDSGVVVKLLEFRRLDINSTAGLPLLLDITAGQORPFLLEKT 223
 OY 226 RVE--GKHVRARRGIDOGGSRMCCROEFVDFREIGWMDWIIQPEGYAMNCTGQCPLH 283
 DB 224 RANPRGAGRARRRTPTEPETPLCCRRDHYVDFOLGMDWIMIQPEGYOLANVCSGCCPH 283
 OY 284 VAGMPCISAFHFAVLNLKANA--AAGTGRGSCCVTSRRPLSLIYDRDSNIYKTDI 341
 DB 284 LAGSPGIAAFHSAVPSFLKANNPFRAGS---SCCVPTARRPLSLIYDHNGNVYKTDV 339
 OY 342 PDWVVEACGS 352
 DB 340 PDWVVEACGS 350

RESULT 8

ID AAF70200 standard; protein: 427 AA.

AA70200;

09-APR-1991 (first entry)

Sequence of porcine inhibin beta-chain precursor beta-A.

Fertility control; contraception; hormone; spermatogenesis.

Sus scrofa domestica.

Key Location/Qualifiers
 Region 1..308
 Protein /note="used to design a long synthetic DNA probe"
 Cleavage-site 309..424
 304..308
 /note="proteolytic processing site"

EP22491-A.

20-MAY-1987.

02-OCT-1986; 86EP-0307586.

12-SEP-1986; 86US-0906729.

03-OCT-1985; 85US-0783910.

10-FEB-1986; 86US-0827710.

(GETH) GENENTECH INC.

Mason AJ, Seeburg PH;

WPI: 1987-137512/20.

N-PSDB: AAN70317.

Recombinant human or porcine inhibin or activin - used for

modulating clinical condition or reproductive physiology of

animals.

Disclosure; Fig 2B; 48pp; English.

A compsn. comprising human or porcine inhibin which is completely
 free of unidentified or porcine proteins is claimed. Also claimed
 are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta
 chain. Sequencing of inhibin-encoding cDNA has led to the
 identification of prodomain regions located N-terminal to the
 mature inhibin chains that represent coordinately expressed
 biologically active polypeptides. The prodomain regions or
 prodomain immunogens are useful in monitoring preproinhibin
 processing in transformant cell culture or in experiments directed
 at modulating the clinical cond. or reproductive physiology of
 animals.

SQ Sequence 427 AA:

Query Match 29.84; Score 550.5; DB 8; Length 427;

Best Local Similarity 31.64; Pred. No. 1.7e-44;

Matches 133; Conservative 68; Mismatches 143; Indels 77; Gaps 10;

OY 6 LLLALFLPTTVVNPRTGCPACWGAIFDLESORELLDLAKKSILDKLS 58
 DB 10 LLASGWIIVRSPTPGSGHSAAPDCSCALATLPKDYVNSQPEVAVKHILMLHLK 69
 OY 59 ORPLTSRPVSRGALKTALRLR-----GPRETLLEHDOKEVEEIIISF 102
 DB 70 KRDPYTOPVPAKALNLAKRLHAKGVNGYVELEDDIGRAEM---NELMEQTSIIITF 126
 OY 103 ADTDLSTINQTRLEFHFSGRMASGMEVOTRMPFVOPFH-NATOT-NNIRVL----- 153
 DB 127 AFAAGTAXXKRLTFEISKEGSDLSYVERAELMLKPKANRTTKTITLFPDOORPQ 186
 OY 154 -----VLRPYDTNLTLTSQYVVOVNASGWYOLLGPEAQAACSGHLLTELVE 202
 DB 187 GSADAGEAEDEGVFPEKSEVLISEKVVDAKSTWHIIPVSSIORLLDQKSLDIRTA 246
 OY 203 SQYAH-----SSLIG-----WFSRRPFAQVYR--VEGKH 231
 DB 247 CEQCHETGASVILGKKKKKEEACGRKRDGACGVDEEKQSHRPLMLQAROSEEHPH 306
 OY 232 RVARRGIDOGGSRMCCROEFVDFREIGWMDWIIQPEGYAMNCTGQCPLHVGMPGIS 291
 DB 307 RRRRRLGECGKVNICKKQKOFVSEKIDIGMDWIMIASGYANANCBEDECPHLAGTSGSS 366
 OY 292 ASFHTAVNLMLKANAAGTGRGSCCVTSRRPLSLIYDRDSNIYKTDI-PDWVVEACGC 351

DB 367 LSHSHVNIHHYMRGHSPPANLKSOCVPTKLPRMSMLYYDDGONIKKDIONMIVEEGC 426

OY 352 S 352

DB 427 S 427

RESULT 9

AAV92017 standard; Protein: 407 AA.

AAV92017:

19-JUL-2000 (first entry)

Human Inhibin B beta subunit.

human inhibin B beta subunit; CKGF; mutant; cysteine knot growth factor;

hairylin loop; infertility.

Homo sapiens.

Location/Qualifiers

/note= "optionally mutated to increase electrostatic

interaction between beta hairylin structure and

a receptor"

Domain 308..328

/label= beta-hairylin_loop-1

/note= "mutant optionally comprises one or more

substitutions in these residues"

Misc-difference 401..407

/note= "optionally mutated to increase electrostatic

interaction between beta hairylin structure and

a receptor"

NO200017360-A1.

30-MAR-2000.

19-MAR-1999; 99MO-US05908.

22-SEP-1998; 98MO-US19772.

(UYMA-) UNIV MARYLAND BALTIMORE.

Weintrub BD, Szkulinski MW;

WPI: 2000-283585/24.

New mutant cysteine knot growth factor proteins comprising one or more

mutant subunits, useful for treating or preventing diseases e.g.

hypothyroidism and thyroid cancer

Claim 298; Page 304; 320pp; English.

This is the wild type human inhibin B beta subunit.

Mutants comprise at least one electrostatic charge altering mutation in a

beta hairylin loop, resulting in increased bioactivity.

Mutant cysteine knot growth factor (CKGF) proteins comprising one or more

mutant subunits and having novel properties or improved pharmacological

properties, compared to wild type CKGFs, are claimed. The CKGF

superfamily comprises at least four families of growth factors: the

glycoprotein hormones, the platelet-derived growth factor (PDGF) family,

CC the neurotrophins and the transforming growth factor-beta family; the

CC families are known to be structurally similar (especially comprising the

CC cysteine knot topology) and it was shown that mutations at certain

CC positions in the CKGF hairylin loops of family members and other members

CC of the CKGF superfamily could significantly alter the biological

CC activities of the CKGF.

CC Mutant transforming growth factor family proteins or analogues are useful

CC for treatment of ovulatory dysfunction, luteal phase defect, unexplained

CC infertility, time-limited conception and in assisted reproduction.

CC Sequence 407 AA:

Query Match 29.6%; Score 548.5; DB 21; Length 407;

Best local Similarity 33.3%; Pred. No. 2.4e-44;

Matches 134; Conservative 66; Mismatches 145; Indels 57; Gaps 13;

OY 2 ASSLLALLFL-----FTTVNKRTEGP-----CPACGALFDLESOREL 42

DB 12 ACULLLAAGMLGPEAWGSPPTPPAAPPPPPGSGSDTCTSCGG---FRPEEL 67

OY 43 -----LIDLAKKSIDKLHSORPILSRVSRGALKTALQRLR-GPRE--TLLEH-- 90

DB 68 GRVDCDFLEAVKRHILSRQMGGRNITHAVKAMVATARKLINGKVRDEGRVEIRPLD 127

OY 91 -----DQREYETISPADTDLSSINOTRLEFHSRGMASMEVROTREFVQ-FPH 142

DB 128 GHASPGADGGERVSEIISPAETDGLASSHVRILYFETISNGONLFFVOASIMLYKLPLP 187

OY 143 -----NATQTNINIVLVLRPDNLTLTSQYVYVNASGYYQLLPENAAOSGHLTLE 198

DB 188 VLEKGRKRVKRVVYVYQEGCHGRMMVKKRVDLKRSQHTPLVEALQALPERKERLN 247

OY 199 LPESQVAHSSLLIGWF-----SHRPFAAQVY-EGKHYRRRGIDCOGSGRMCCRQE 251

DB 248 LDVQDCSCQGLAVVPVYVQGESHRPFYVQARLGDSSHRIKRGLECDGRTNLCRQO 307

OY 252 FVVDREIIGNDMIIOPEGYAMNCTGQCPRLHVAQPGISASFHTAVNLKANAA-AGT 310

DB 308 FFIDFRILGNDMIIVPTGYGYGVCSPAYLAGVSGSFRHVAVVOYRMRLNGT 367

OY 311 TGRSGCCVPTSRRLSLIYDRDSNIVKTDIPMVEACGS 352

DB 368 V--NSCCTPKLSTMSMLYFDDEYNIVKRDVPMIVEEGCA 407

RESULT 10

AAV92019

ID AAV92019 standard; Protein: 407 AA.

AAV92019:

19-JUL-2000 (first entry)

Human activin B subunit.

human activin B subunit; CKGF; mutant; cysteine knot growth factor;

hairylin loop; infertility.

Homo sapiens.

Location/Qualifiers

/note= "optionally mutated to increase electrostatic

interaction between beta hairylin structure and

a receptor"

Domain 308..328

/label= beta-hairylin_loop-1

/note= "mutant optionally comprises one or more

substitutions in these residues"

Misc-difference 329..375

/note= "optionally mutated to increase electrostatic

interaction between beta hairylin structure and

a receptor"

OY 26 CPACWGAIFDLESREL-----LDDAKKSLIDKHLISORPLISRPVSGALKTALORL 79
 DB 1 CTSCGG-----FRREELGRVDGDFLEAVKRRHLSRLQMRGRPNTHAVPAAMVATLRKL 56
 OY 80 R-GPRE-----TLLEH-----DOROEYEIISFADTLLSINOTRLEPHFSGRMASG 126
 DB 57 HAGKREGRREVEIRHLDHASPACDGGGRVSEIISFAETDLASSRRLVFFISNEGQON 116
 OY 127 MEVROTREFEYQ-FPH-----NATOTNIRVLYLRPYDTNLTLSOVVYNASGWYQL 181
 DB 117 LRVVQASLMLYKLLPYVLEKSGRRKRVKVFQDQGHGDMNVEKRVDLKRSQWHITFP 176
 OY 182 LCPBAQACSGCHLTLELVPEESQVHSSLLIGWF-----SHRPFVAQVRV-EGKHVR 234
 DB 177 LTRVATDALFERREBRRLNDVOCDSQELAVVPVFDPEESHREPFVYVQARLQDSRRHRIR 236
 OY 235 RRGIDCGGSRMCROEFFVDREIGNDMIIOPEGYAMNCTGOCPLHVAGMPGISASF 294
 DB 237 KRGLCEDGRNLCRQOFFIDFRLIGNDMIIAPGYGNVCEGSPAVLAGVPSASAF 296
 OY 295 HTAVMLKLANMA-AGTGRGSCCVPTSRRLPLLYDRDSNIVKTDIPDMVVEACGCS 352
 DB 297 HTAVNVMYRRKGLNPCTV--NSCCTFKLSTMSMLYFDEYNIIVKRDVPMIIVECGCA 353

RESULT 12
 AAF70203 standard; protein: 426 AA.
 ID AAF70203

AC AAF70203;

DT 09-APR-1991 (first entry)

XX Sequence of human inhibin beta-chain precursor beta-A.

KM Fertility control; contraception; hormone; spermatogenesis.

XX Homo sapiens.

OS Location/Qualifiers

FT Modified-site 165..167 /note="potential N-linked glycosylation sites"

FT Region 1..28 /note="signal sequence"

FT Region 28..310 /note="pro region"

FT Protein 311..326 /note="pro region"

FT Cleavage-site 306..310 /note="proteolytic processing site"

FT EP222491-A.

PN 20-MAY-1987.

XX 02-OCT-1986; 86EP-0307586.

PR 12-SEP-1986; 86US-0906729.

PR 03-OCT-1985; 85US-0783910.

PR 10-FEB-1986; 86US-0827710.

XX (GETH) GENENTECH INC.

XX Mason AJ, Seeburg PH;

XX WPI; 1987-137512/20.

XX N-PSDB: AAN70315.

XX Recombinant human or porcine inhibin or activin - used for

XX modulating clinical condition or reproductive physiology of

XX animals.

XX Disclosure: Fig 8A: 48pp: English.

CC A compsn. comprising human or porcine inhibin which is completely
 CC free of unidentified or porcine proteins is claimed. Also claimed
 CC are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta
 CC chain. Sequencing of inhibin-encoding cDNA has led to the
 CC identification of prodomain regions located N-terminal to the
 CC mature inhibin chains that represent coordinately expressed
 CC biologically active polypeptides. The prodomain regions or
 CC prodomain immunogens are useful in monitoring preproinhibin
 CC processing in transformant cell culture or in experiments directed
 CC at modulating the clinical cond. or reproductive physiology of
 CC animals.

SO Sequence 426 AA;

Query Match 29.2%; Score 540; DB 8; Length 426;

Best Local Similarity 31.2%; Pred. No. 1,7e-43; Mismatches 139; Indels 82; Gaps 11;

Matches 132; Conservative

OY 6 LIALFLPTPTVVPKTEG-----PCPACWGAIF--DLESRELLDLDLAKKSLIDKHLIS 58
 DB 10 LLASCMIVVSSPTPGSEGHSAAPDCPCALALPRKDVPSOPEVNEAVKHHILMLHLK 69
 OY 59 QRPILSRPYSRGALKTALQRLR-----GPRRETLLEHDOQEYEIISF 102
 DB 70 KRPDVTPVPKALALNAIRKLHVGKGVNGYVIEDDIGHRAEM--NELMEQTSIITFP 126
 OY 103 ADPDLSSINQTRLEPHFSGRMASGMEVROTREFEYQFPH-NATOT-NINIRVLYLRPY-- 158
 DB 127 AE--SCTARKTLHFEISKEGSDLSVERAEVWLFLEKVRARTKRYTIRLEQCKHPQ 183
 OY 159 -----DTNLTLSOVVYNASGWYQLLGPEAQACSGCHLTLEL--- 199
 DB 184 GSLDTGEAEVGLKGRSELSEKVVYDARKSTWIVFYSSSIQPLDQKSSLDVRLA 243
 OY 200 VPESQVHSSLLI-----GMSRRPFVAQVRV-VBG 229
 DB 244 CEQCOESGASLYLKKKKKEEGEGCKKGGGCGAGADEKEOSHRPFLMLQARQSEDH 303
 OY 230 KHRVRRGIDCGGSRMCROEFFVDREIGNDMIIOPEGYAMNCTGOCPLHVAGMPG 289
 DB 304 PHRRRRRLCECDGVNICKCKKQFFVSFKDIGNDMIIAPGYGNVCEGSPAVLAGVPS 363
 OY 290 ISASPHFVAVMLKLANMAAGTGRGSCCVPTSRRLPLLYDRDSNIVKTDIPDMVVEAC 349
 DB 364 SLSFHSYVINHYRMGRGSPFANLKSOCVPTKLPMSMLYDDGQNIKKIDQNIIVEEC 423
 OY 350 GCS 352
 DB 424 GCS 426

RESULT 13

AAV92016 standard; protein: 426 AA.

ID AAV92016

XX 19-JUL-2000 (first entry)

XX Human inhibin A beta subunit.

XX human inhibin A beta subunit; CKGF; mutant; cysteine knot growth factor;

XX hairpin loop; infertility.

XX Homo sapiens.

XX Location/Qualifiers

XX Key 1..325 /note="optionally mutated to increase electrostatic

XX interaction between beta hairpin structure and

XX a receptor"

XX Domain 326..346

XX /label="beta_hairpin_loop-1"

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FT      /note- "mutant optionally comprises one or more
FT      substitutions in these residues."
FT      Misc-difference 347..394
FT      /note- "optionally mutated to increase electrostatic
FT      interaction between beta hairpin structure and
FT      a receptor"
FT      Domain
FT      395..419
FT      /label= beta_hairpin_loop_3
FT      /note- "mutant optionally comprises one or more
FT      substitutions in these residues"
FT      Misc-difference 420..426
FT      /note- "optionally mutated to increase electrostatic
FT      interaction between beta hairpin structure and
FT      a receptor"
FT      WO200017360-A1.
FT      PD
FT      30-MAR-2000.
FT      PF
FT      19-MAR-1999: 99WO-US05908.
FT      XX
FT      22-SEP-1998: 98WO-US19772.
FT      PA
FT      (UYMA-) UNIV MARYLAND BALTIMORE.
FT      PI
FT      Weintraub BD, Szklutinski MM;
FT      DR
FT      WPI: 2000-283585/24.
FT      PT
FT      New mutant cysteine knot growth factor proteins comprising one or more
FT      mutant subunits, useful for treating or preventing diseases e.g.
FT      hypothyroidism and thyroid cancer
FT      PS
FT      Claim 283: Page 303: 320pp: English.
CC      This is the wild type human inhibin A beta subunit.
CC      Mutants comprise at least one electrostatic charge altering mutation in a
CC      beta hairpin loop, resulting in increased bioactivity.
CC      Mutant cysteine knot growth factor (CKGF) proteins comprising one or more
CC      mutant subunits and having novel properties or improved pharmacological
CC      properties, compared to wild type CKGFs, are claimed. The CKGF
CC      superfamily comprises at least four families of growth factors: the
CC      glycoprotein hormones, the platelet-derived growth factor (PDGF) family,
CC      the neurotrophins and the transforming growth factor-beta family; the
CC      families are known to be structurally similar (especially comprising the
CC      cysteine knot topology) and it was shown that mutations at certain
CC      positions in the CKGF hairpin loops of family members at certain
CC      of the CKGF superfamily could significantly alter the biological
CC      activities of the CKGF.
CC      Mutant transforming growth factor family proteins or analogues are useful
CC      for treatment of ovulatory dysfunction, luteal phase defect, unexplained
CC      infertility, time-limited conception and in assisted reproduction.
CC      XX
SQ      Sequence 426 AA:
Query Match 29 28: Score 540: DB 21: Length 426:
Best local similarity 31.28: Pred. No. 1.7e-43:
Matches 132: Conservative 70: Mismatches 139: Indels 82: Gaps 11:
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OY      59 ORPILSRPVSKALKTALORLR-----GPRRETLLEHDQOEYEIISF 102
DB      70 KRDVTPQPKAALLNALIKLHVGVGNGVEIEDDGRANEM---NELMEQSEITTF 126
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DB      127 AE---SGTARKLHFIEIKESGDSLVBRAEVWLFKVPKANKRRTVTIRLFQOQKHPO 183
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DB      184 GSLDTGEAEVGLKGERSELLSEKVVYDARKSTWVFPVSSISQRLDQGKSLDVR1A 243
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DB      244 CEQCQESGASLVLLGKKKKKEEGECKKKGGGAGADEKEQSHRPLMLQARQSEDH 303
OY      230 KHRVRRRGICCGGSRNCCQEFFVDREIGNDWIIQPEGYAMNFCGCPPLHVAQMG 289
DB      304 PHRRRRGLCDGKVNICKCKKQFFVSFKDIGNDWIIAPSGYHANYCEGECPSH1AGTSG 363
OY      290 ISASFHTAVLNLKANAAGTTGSCCVPTSRPRLIYDRDNIYKTDIPDMVNEAC 349
DB      364 SLSLFSHTVINHYRMGHSFANLKCSCVPTLRPMKMLYTDGONIIKKDIQNMIVREC 423
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DB      424 GCS 426
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ID      AA92018 standard: Protein: 426 AA.
AC      AA92018;
DT      19-JUL-2000 (first entry)
DE      Human activin A subunit.
XX      human activin A subunit.
XX      human activin A subunit; CKGF; mutant; cysteine knot growth factor;
XX      hairpin loop; Infertility.
XX      OS
XX      Homo sapiens.
XX      Key
XX      Location/Qualifiers
FT      Misc-difference 1..325
FT      /note- "optionally mutated to increase electrostatic
FT      interaction between beta hairpin structure and
FT      a receptor"
FT      Domain
FT      326..346
FT      /label= beta_hairpin_loop_1
FT      /note- "mutant optionally comprises one or more
FT      substitutions in these residues"
FT      Misc-difference 347..394
FT      /note- "optionally mutated to increase electrostatic
FT      interaction between beta hairpin structure and
FT      a receptor"
FT      Domain
FT      395..419
FT      /label= beta_hairpin_loop_3
FT      /note- "mutant optionally comprises one or more
FT      substitutions in these residues"
FT      Misc-difference 420..426
FT      /note- "optionally mutated to increase electrostatic
FT      interaction between beta hairpin structure and
FT      a receptor"
FT      WO200017360-A1.
FT      PD
FT      30-MAR-2000.
FT      PF
FT      19-MAR-1999: 99WO-US05908.
FT      XX
FT      22-SEP-1998: 98WO-US19772.
FT      PA
FT      (UYMA-) UNIV MARYLAND BALTIMORE.
FT      PI
FT      Weintraub BD, Szklutinski MM;
FT      DR
FT      WPI: 2000-283585/24.
FT      PT
FT      New mutant cysteine knot growth factor proteins comprising one or more
FT      mutant subunits, useful for treating or preventing diseases e.g.
FT      hypothyroidism and thyroid cancer

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Homo sapiens.

Job time : 43 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 12, 2002, 02:05:12 : Search time 15.5 Seconds
(Without alignments)
554.697 Million cell updates/sec

Title: US-09-684-383-4

Perfect score: 1850
Sequence: 1 MASSLLALLFLFPTTVNP.....DSNIVKTDIPDMVFAAGCS 352

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents-AA:

- 1: /cgn2_6/ptodata/1/laa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/laa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/laa/6A.COMB.pep.*
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- 5: /cgn2_6/ptodata/1/laa/PTCUS.COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1850	100.0	352	4	US-09-218-176-4
3	1398	75.6	352	1	US-08-482-577B-2
4	1398	75.6	352	3	US-08-289-222E-4
5	1398	75.6	352	4	US-09-218-176-2
6	1398	75.6	352	2	US-09-054-526B-4
7	594	32.1	350	4	US-08-765-662-14
8	594	32.1	350	5	PCT-US95-08745-14
9	558	30.2	106	1	US-08-482-577B-24
10	558	30.2	106	3	US-08-289-222E-28
11	558	30.2	106	4	US-09-218-176-7
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17	543	29.4	353	1	US-08-459-850-43
18	543	29.4	353	1	US-08-459-214-43
19	543	29.4	424	1	US-08-197-792-31
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21	543	29.4	424	1	US-08-459-214-31
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23	540	29.2	426	1	US-08-459-850-41
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25	460	24.9	137	1	US-08-455-550-11
26	444	24.0	119	2	US-08-374-215A-12
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31	401.5	21.7	121	1	US-08-581-529B-18	Sequence 18, Appl
32	401.5	21.7	121	1	US-08-455-559-24	Sequence 24, Appl
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42	396	21.4	122	1	US-08-455-559-23	Sequence 23, Appl
43	396	21.4	122	2	US-08-525-596B-27	Sequence 27, Appl
44	396	21.4	122	2	US-08-581-528A-17	Sequence 17, Appl
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ALIGNMENTS

RESULT 1
US-08-482-577B-4
Sequence 4, Application US/08482577B
Patent No. 5807713
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY, AND ORAM
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,577B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, SHARON
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P564-5010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
DOCUMENT NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
US-08-482-577B-4
Query Match 100.0%; Score 1850; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.3e-174;

Matches 352: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 301 LKANAAGTTGRGSCCVPSTRPLSLLYDRDSNIVKTDIPDMVVEACGCS 352

RESULT 2
 US-09-218-176-4
 ; Sequence 4, Application US/09218176
 ; Patent No. 6171584
 ; GENERAL INFORMATION:
 ; APPLICANT: H TTEN, Gertrud
 ; APPLICANT: NEIDHARDT, Helge
 ; APPLICANT: BECHTOLD, Rolf
 ; APPLICANT: POHL, Jens
 ; APPLICANT: PAULISIA, Michael
 ; TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
 ; TITLE OF INVENTION: TGF- FAMILY
 ; NUMBER OF SEQUENCES: 49
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP
 ; STREET: 655 FIFTEENTH STREET, N. W., G Street Lobby,
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC COMPATIBLE
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/218,176
 ; FILING DATE: Herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/679,048
 ; FILING DATE: 12-JUL-1996
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP96/03065
 ; FILING DATE: 12-JUL-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP93/00350
 ; FILING DATE: 2-FEB-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/482,577
 ; FILING DATE: 7-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 92 102 324,8
 ; FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE P 44 23 190,3
 ; FILING DATE: 01-JUL-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE 195 11 243,1
 ; FILING DATE: 27-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KITTS, Monica Chin
 ; REGISTRATION NUMBER: 36,105
 ; REFERENCE/DOCKET NUMBER: P564-6010
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202/638-5000
 ; TELEFAX: 202/638-4810
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 352 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-218-176-4

Query Match 100.0%; Score 1850; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1,3e-174;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASSLLALLFLPTTVNPKTEGPCACGATFDESORELLDLAKKSILDKLHLSOR 60
 DB 1 MASSLLALLFLPTTVNPKTEGPCACGATFDESORELLDLAKKSILDKLHLSOR 60
 QY 61 PILSRPVSRGALKTAQRLRGPRRETLLEHDOREYEIISFADTDLSSINOTRLEPHFS 120
 DB 61 PILSRPVSRGALKTAQRLRGPRRETLLEHDOREYEIISFADTDLSSINOTRLEPHFS 120
 QY 121 GRMASGMEVROTRMFEPVOPHNATOTMNI RVLRLPYDTNLTLTSQYVVOVNASGWYOL 180
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 QY 241 QGGSRMCCROEFFVDPREIGNDWIIQPEGYAMNCTGQCPLHVAGMPCISASFTAVLN 300
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 ; Sequence 2, Application US/08482577B
 ; Patent No. 5807713
 ; GENERAL INFORMATION:
 ; APPLICANT: HOTTEN, GERTRUD
 ; APPLICANT: NEIDHARDT, HELGE
 ; APPLICANT: BECHTOLD, ROLF
 ; APPLICANT: POHL, JENS
 ; TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
 ; TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
 ; NUMBER OF SEQUENCES: 49
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY, AND ORAM
 ; STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,
 ; CITY: SUITE 330
 ; CITY: WASHINGTON
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk


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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,577B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, SHARON
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P564-5010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-577B-2

Query Match
Best Local Similarity 76.2%; Score 1398; DB 1; Length 352;
Matches 269; Conservative 32; Mismatches 50; Indels 2; Gaps 2;

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DB 1 MTSSLLAFLAFLPTTVVNPKEGPCPCACGAFIDLESORELLDLAKKSILDKLHLSOR 60
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DB 61 PTLNRPVSRALTAQLRGRPRELLEHDOREYEYIIISPAVDLSINOTRLEPHFS 120
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DB 300 NLKANAAGTTGSGCCVPTSRRLSLLYYDRDSNIVKTDIPDMVVEACGCS 352

RESULT 4
US-08-289-222E-4
Sequence 4, Application US/08289222E
Patent No. 6120760
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: POHL, JENS
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY F. ORAM
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,222E
FILING DATE: 25-AUG-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-289-222E-4

Query Match
Best Local Similarity 76.6%; Score 1398; DB 3; Length 352;
Matches 269; Conservative 32; Mismatches 50; Indels 2; Gaps 2;

QY 1 MASSLLALLFLPTTVVNPKEGPCPCACGAFIDLESORELLDLAKKSILDKLHLSOR 60
DB 1 MTSSLLAFLAFLPTTVVNPKEGPCPCACGAFIDLESORELLDLAKKSILDKLHLSOR 60
QY 61 PILSRVSRGALTAQLRGRPRELLEHDOREYEYIIISPAVDLSINOTRLEPHFS 120
DB 61 PTLNRPVSRALTAQLRGRPRELLEHDOREYEYIIISPAVDLSINOTRLEPHFS 119
QY 121 G-RNASGMEVROTFRMFVQFPNNATOTMIRVLYLRPYDTNLTLSQVYVGNASGMWQ 179
DB 120 SDRTAGREVOQASLMFVQLPSTNTWTLKRVYLVGPHNTNLTATQYLLLEVDASGMHQ 179
QY 180 LLLGPEAOACSGOHLTLELVPSOVYHSSLLIGMFSHRPFVAAYQVREGKHRRRGID 239
DB 180 LPLGPEAOACSGOHLTLELVPSOVYHSSLLIGMFSHRPFVAAYQVREGKHRRRGID 239
QY 240 CQGSRRMCCROEFFVDREIGMNDWIIIOPEGYAMNFCIGCCPLHVGMGISASFTAVL 299
DB 240 CQGSRRMCCROEFFVDREIGMNDWIIIOPEGYAMNFCIGCCPLHVGMGISASFTAVL 299
QY 300 NLKANAAGTTGSGCCVPTSRRLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
DB 300 NLKANAAGTTGSGCCVPTSRRLSLLYYDRDSNIVKTDIPDMVVEACGCS 352

RESULT 5
US-09-218-176-2
Sequence 2, Application US/09218176
Patent No. 6171584
GENERAL INFORMATION:
APPLICANT: H TTEN, Gertrud
APPLICANT: NEIDHARDT, Helge
APPLICANT: BECHTOLD, ROLF

```

APPLICANT: POHL, Jens
APPLICANT: PAULISTA, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
TITLE OF INVENTION: TGF- FAMILY
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESS: NIKAI, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., G Street Lobby,
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218,176
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,048
FILING DATE: 12-JUL-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03065
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 2-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,577
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92 102 324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 11 243.1
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, Monica Chin
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-6010
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-218-176-2

Query Match 75.6%; Score 1398; DB 4; Length 352;
Best Local Similarity 76.2%; Pred. No. 5.6e-130;
Matches 269; Conservative 32; Mismatches 50; Indels 2; Gaps 2;

QY 1 MASSLLALLFLPTTVVNPKEGCPACMGAIPTDLESQRRLDLDAKSLIDKLHLR 60
DB 1 MSSLLALLFLPTTVVNPKEGCPACMGAIPTDLESQRRLDLDAKSLIDKLHLR 60
QY 61 PILSRPVSGALKTALORLGRPRRTLEHDOQOEVEIISFADTDLSSINOTLEPHFS 120
DB 61 PILSRPVSGALKTALORLGRPRRTLEHDOQOEVEIISFADTDLSSINOTLEPHFS 119
QY 121 G-RMASGNEVROTREMFVQFPFHNAOTGMNIRVLVLRPYDTNLTLSQYVQVWASGWO 179

DB 120 SDRTAGDREVOQASLMFVQLPSTWTTLKRVYLGLPHTNLTFLATVLLVEDASGMHQ 179
QY 180 LILGPEAOACSGHLLTELVPESOVAHSSILIGWFSHREFAAOVRVGRKRVRRGID 239
DB 180 LPLGPEAOACSGHLLTELVPESOVAHSSILIGWFSHREFAAOVRVGRKRVRRGID 239
QY 240 CQGSRMCCROEFVDFEIGMNDMTIOPEGYAMNCTGCPPLHVAMGSIASFHTAVL 299
DB 240 CQGSRMCCROEFVDFEIGMNDMTIOPEGYAMNCTGCPPLHVAMGSIASFHTAVL 299
QY 300 NLKANAAGTTGRCSCCVPTSRPLSLYDDDSNIVTIDPDVVEACGS 352
DB 300 NLKANAAGTTGRCSCCVPTSRPLSLYDDDSNIVTIDPDVVEACGS 352

RESULT 6
US-09-054-526B-4
Sequence 4; Application US/09054526B
Patent No. 6197550
GENERAL INFORMATION:
APPLICANT: H TTE, GERTH
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESS: NIKAI, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,526B
FILING DATE: 03-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-8005
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-054-526B-4

Query Match 75.6%; Score 1398; DB 4; Length 352;

Best Local Similarity 76.2%; Pred. No. 5.6e-130;
Matches 269; Conservative 32; Mismatches 50; Indels 2; Gaps 2;

QY 1 MASSLLALLFLPTPTVYVNPKEGRCPCAKCAIFDLESQRELLDLAKKSLDKLHLSOR 60
DB 1 MSSLFLFLFLPTVTVPRAGGCGPGLTSLQRELLDLAKKSLDKLHLSOR 60
QY 61 PLSHPVSGALKTALQRLGRPRRETLLEHDOBOEVEIISFADTDLSSINOTRLEHPS 120
DB 61 PLNRPVSRALRTALQHLHGVGOCALLE-DNREOECIISFATGISTINOTRLEHPS 119
QY 121 G-RMASCHEVROTRPMFVQPRHATOTMIRVLYLRPYDTNLTLSQYVVOVNASGMYQ 179
DB 120 SORTAGREVQOASLAFVQLPSNTWTALKVRLVGLGPHNLTALQYLEVDASGMYQ 179
QY 180 LLLGPEAQAACSGHLLTELVEPVASHSLLGMSHPRPVAAOVVEGHRVRRCID 239
DB 180 LPLGPEAQAACSGHLLTELVEPVASHSLLGMSHPRPVAAOVVEGHRVRRCID 239
QY 240 CCGSRMCCROEPFVDFEIGNDWIIOPEGYAMNCTGCPPLHVGMPGISAFHTAVL 299
DB 240 CCGSRMCCROEPFVDFEIGNDWIIOPEGYAMNCTGCPPLHVGMPGISAFHTAVL 299
QY 300 NELKANAAGTTGRGSCCVPTSRPLSLLYDRDSNIYKTDIPMVEACGCS 352
DB 300 NELKANAAGTTGRGSCCVPTSRPLSLLYDRDSNIYKTDIPMVEACGCS 352

RESULT 7
US-08-765-662-14
Sequence 14, Application US/08765662
Patent No. 5929213

GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 4225 Executive Square, Suite 1400

CITY: LA JOLLA

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/765,662

FILING DATE: 28-APR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/08745

FILING DATE: 12-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hallie, Ph.D., Lisa A

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/042M01 (FD-3830)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-678-5070

TELEFAX: 619-678-5099

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 350 amino acids

TYPE: amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:
US-08-765-662-14

Query Match 32.1%; Score 594; DB 2; Length 350;
Best Local Similarity 39.3%; Pred. No. 1.3e-50;
Matches 141; Conservative 51; Mismatches 109; Indels 56; Gaps 11;

QY 22 TEGPCPACWGAIFDLESQRELLDLAKKSLDKLHLSORPLSHPSRGALKTALQRLR- 80
DB 22 TGVPCPCGSGSLAPARALVYLELAKQOILIDGLHLSRPRITHPPQALTRALRLQRP 81
QY 81 ---GPRRETLLEHDOBOEVEIISFAD-TDLSSINOTRLEHPSGRRASGMEVROTRFME 136
DB 82 GSVAENGE-----EVISFATVTDSTSAVSSILTFHLS--TPRSHHLYHAALWL 128
QY 137 FVQPHNATOTMNI-----RVLYVRPYDTNLTLSQYVVOVNASGMYQTLIGP 184
DB 129 HVLPLPTGLCTRIRKQPRRRRQGSRTLLAEHNTLN-----GNIITLTPS 175
QY 185 EAQAACSGHLLTELVEPVASHSLLGMSHPRPVAAOVVEGHRVRRCID 235
DB 176 SGLRGKSGVLKQLDCHPRLEGNSTVTGQPRRLDVTAGHOQPFLEKIRANERQAGRAR 235
QY 236 RGIDCGSRMCCROEPFVDFEIGNDWIIOPEGYAMNCTGCPPLHVGMPGISAFHTAVL 295
DB 236 RPTCEPATPLCCRRDHYVDFEIGNDWIIOPEGYAMNCTGCPPLHVGMPGISAFHTAVL 295
QY 296 TAVNLNKKANA--AAGTTGRGSCCVPTSRPLSLLYDRDSNIYKTDIPMVEACGCS 352
DB 296 SAVFSLLKANMPAST-----SCVPTARPLSLLYDRDSNIYKTDIPMVEACGCS 350

RESULT 8
PCT-US95-08745-14

Sequence 14, Application PC/TUS9508745

GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 4225 Executive Square, Suite 1400

CITY: LA JOLLA

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/08745

FILING DATE: 12-JUL-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Hallie, Ph.D., Lisa A

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/042M01 (FD-3830)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-678-5070

TELEFAX: 619-678-5099

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 350 amino acids

TYPE: amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:
PCT-US95-08745-14

Query Match 32.1% Score 594; DB 5; Length 350;
Best Local Similarity 39.3% Pred. No. 1.3e-50;
Matches 141; Conservative 51; Mismatches 109; Indels 58; Gaps 11;

QY 22 TEGCPACWAIPEDESORELLDLAKSIIDKLSQRPILSPVSGALKTALRLR- 80
DB 22 TGSVCPSGSGKLAPOARALVLELAKQOILDHLTSRPITHPPQALTRALRLR- 81
QY 81 --GPRRTLEHQROEEVEIISFAD-TDLSSTNORLEHPSGMAAGMEVNOTPFMF 136
DB 82 GSVAPGCE-----EVSFAVYDSTSAVSSLLTFHLS--TPRSHHLYHARLWL 128
QY 137 FVQPPHATOTMTI-----RVLYLRPYDTNLTLSQVYVGVNAGWYOLLGP 184
DB 129 HVLPTLPTGLCLRFHMGPRRRRSGSRTLLAEHITNL-----GHTTLTLP 175
QY 185 EAQACSGCHLTLELVESOVANSSL-----ILGWFSH-RPPVAAQVVE--GKHVR 235
DB 176 SGLRSGSVLKLQDLDRPLEGNSVTGQPRRLDITAGHOQPLELKI RANEPGAGRARR 235
QY 236 RGIDCGGSRMCCROEPFVDFREIGWMDMIIOPGVAMNCTGQCPLHVGAMGISA 235
DB 236 RPTCEPATPLCCRRDHYVDQELGMHMDWILQPEGTQVLTNCSGCCPHLAGSP 235
QY 296 TAVINLLKANA--AAGTTGSGSCVPTSRRLSLLYDRDSNIVKTDIPDMV 352
DB 296 SAVESLLKANNPMFST-----SCCVPTARRPLSLLYLDHNGNVKTDIPDMV 350

RESULT 9
US-08-482-577B-24

Sequence 24, Application US/08482577B
Patent No. 5807713
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY, AND ORAM
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/482.577B
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, SHARON
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P564-5010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-4810
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-577B-24

Query Match 30.2% Score 558; DB 1; Length 106;
Best Local Similarity 93.4% Pred. No. 8.6e-48;
Matches 99; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 247 CCHOEFVDFREIGWMDMIIOPGVAMNCTGQCPLHVGAMGISAFTAVINLLKANA 306
DB 1 CCHOEFVDFREIGWMDMIIOPGVAMNCTGQCPLHVGAMGISAFTAVINLLKANA 60
QY 307 AAGTTGSGSCVPTSRRLSLLYDRDSNIVKTDIPDMV 352
DB 61 AAGTTGSGSCVPTARRPLSLLYLDHNGNVKTDIPDMV 106

RESULT 10
US-08-289-222E-28

Sequence 28, Application US/08289222E
Patent No. 6120760
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-
TITLE OF INVENTION: FAMILY
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY & ORAM
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/289.222E
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-289-222E-28

Query Match 30.28; Score 558; DB 3; Length 106;
Best Local Similarity 93.48; Pred. No. 8.6e-48;
Matches 99; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 247 CCR0EFFVDPRFIGNMDIIOPEGYAMNFCGOCPLHVAGMPGISAFHVALNLLKANA 306
DB 1 CCR0EFFVDPRFIGNMDIIOPEGYAMNFCGOCPLHVAGMPGISAFHVALNLLKANT 60

OY 307 AAGTGGSCCVPTRARPLSLIYDRDSNIYKTDIPMVVEACCS 352
DB 61 AAGTGGSCCVPTRARPLSLIYDRDSNIYKTDIPMVVEACCS 106

RESULT 11
US-09-218-176-7
Sequence 7, Application US/09218176
Patent No. 6171584
GENERAL INFORMATION:
APPLICANT: H. TITEN, Gertrud
APPLICANT: NEIDHARDT, Helge
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, Jens
APPLICANT: PAULISTA, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
TITLE OF INVENTION: TGF- FAMILY
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G Street lobby,
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218.176
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03065
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 2-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,577
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92 102 324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 11 243.1
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, Monica Chin
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-6010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-218-176-7

Query Match 30.28; Score 558; DB 4; Length 106;
Best Local Similarity 93.48; Pred. No. 8.6e-48;
Matches 99; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 247 CCR0EFFVDPRFIGNMDIIOPEGYAMNFCGOCPLHVAGMPGISAFHVALNLLKANA 306
DB 1 CCR0EFFVDPRFIGNMDIIOPEGYAMNFCGOCPLHVAGMPGISAFHVALNLLKANT 60

OY 307 AAGTGGSCCVPTRARPLSLIYDRDSNIYKTDIPMVVEACCS 352
DB 61 AAGTGGSCCVPTRARPLSLIYDRDSNIYKTDIPMVVEACCS 106

RESULT 12
US-09-054-526B-28
Sequence 28, Application US/09054526B
Patent No. 6197550
GENERAL INFORMATION:
APPLICANT: H. TITEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054.526B
FILING DATE: 03-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-8005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid

STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-054-5268-28

Query Match 30.2%; Score 558; DB 4; Length 106;
Best Local Similarity 93.4%; Pred. No. 8.6e-48;
Matches 99; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 247 CCROEFVDFREIGWMDMIIOPEGYAMFCTGOCPLHVGMPGISASFHTAVILKAM 306
DB 1 CCROEFVDFREIGWMDMIIOPEGYAMFCTGOCPLHVGMPGISASFHTAVILKAM 60
QY 307 AAGTGRSGCCYPTSRRLSLTYDROSNIVKTDIPDMVYACGCS 352
DB 61 AAGTGGGSCCVPARRLSLTYDROSNIVKTDIPDMVYACGCS 106

RESULT 13
US-08-197-792-33

Sequence 33, Application US/08197792

Patent No. 5525488

GENERAL INFORMATION:

APPLICANT: Anthony J. Mason

APPLICANT: Peter H. Seeburg

TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or Beta Chains of Inhibin and

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/197,792

FILING DATE: 16-FEB-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/958414

FILING DATE: 08-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/744207

FILING DATE: 12-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/215466

FILING DATE: 05-JUL-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 06/906729

FILING DATE: 31-DEC-1986

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 06/827710

FILING DATE: 07-FEB-1986

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 06/783910

FILING DATE: 03-OCT-1985

ATTORNEY/AGENT INFORMATION:

NAME: Hasak, Janet E.

REGISTRATION NUMBER: 28,616

REFERENCE/DOCKET NUMBER: 29/P204

TELEPHONE: 415/225-1896

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 349 amino acids

TYPE: amino acid

TOPOLOGY: linear
US-08-197-792-33

Query Match 29.5%; Score 546; DB 1; Length 349;
Best Local Similarity 35.8%; Pred. No. 7.1e-46;
Matches 120; Conservative 65; Mismatches 122; Indels 28; Gaps 9;

QY 44 LDLAASLIDLDLHLSQRIISRPVSRALKTALQRLR-GPRRE---TLLEH-----90
DB 17 LEAVRHILNRLQMGKGRNITHAVPKAMVYALJLKHAGVREDGRVEIPHLGHASPCA 76
QY 91 DQREVEEIIISFADTDLSSINOTRIEFHFGSRMASGMEVROTFRMFYQ-FPH---NAT 145
DB 77 DQERVSEIISFAETDGLASSRVALYFFISNEGQNLFFVQASLMLYLKLPVLEKGR 136
QY 146 QTMNIRVLVLRPYDTNLTLSQVYVQVNASGWYQLLGPEQAACSGQHLTLEVPESQV 205
DB 137 RKVRKVVYFQEPGHGDMVDVEKRVDLKRSQWHTLPLTEAIOALPFRGERLNLDOQCG 196
QY 206 AHSLLIGMF-----SHRPEVAAQVRV-EGKHVRVRRGIDCGGRMCCROEFVDFRE 258
DB 197 COELAVVPEVDFPEESHRRPEVVOARLGDSRRIRKRGLEDGRNLLCCROOFFIDFRL 256
QY 259 IGWMDMIIOPEGYAMFCTGOCPLHVGMPGISASFHTAVILKAMAA-AGTGRSGCC 317
DB 257 IGWMDMIIPGYGYNCEGSCPAVLACVPGASSFHTAVVNOYRMRGILNPQTIV--NSCC 314
QY 318 VPTSRRLSLTYDROSNIVKTDIPDMVYACGCS 352
DB 315 IPTKLSTMSMLYFDEYVIVKRDVPMNIVECCCA 349

RESULT 14
US-08-459-850-33

Sequence 33, Application US/08459850

Patent No. 5665568

GENERAL INFORMATION:

APPLICANT: Anthony J. Mason

APPLICANT: Peter H. Seeburg

TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or

TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypept

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,850

FILING DATE: 02-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/197792

FILING DATE: 17-FEB-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/958414

FILING DATE: 08-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/744207

FILING DATE: 12-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/215466

FILING DATE: 05-JUL-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 06/906729

FILING DATE: 31-DEC-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/827710
FILING DATE: 07-FEB-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/783910
FILING DATE: 03-OCT-1985
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 297205
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
TOPOLOGY: Linear
US-08-459-850-33

Query Match 29.5%, Score 546, DB 1, Length 349;
Best Local Similarity 35.8%, Pred. No. 7,1e-46;
Matches 120; Conservative 65; Mismatches 122; Indels 28; Gaps 9;

44 IDLAKSLIDKHLISORPLSPVSGALKTALORLR-GPRRE--TLEH----- 90
17 LEAVRHLNRLQMGKRPITHAVPKAMVTLAKRLHAGKYREDGRVEIPHLDGHASGCA 76
91 DOROEVEIISFADTDLSSINOTRLEFHSGRMASGMEVROTFRMFVQ-FPH---NAT 145
77 DQGERVSEIISFAETDGLASSRVRLYFISNGNQLFVVOASLMLYLKLLPYVLEKSR 136
146 QTMNIRVLYRPTDNLITLSQYVYVQVNASGYOLLGPEAOACSGOHLTLEVPESOV 205
137 RRVKRVYVQEPGHDGRDVEKRVDLKRSQWHTLPLEATQALFERGERRLNLDVQCDG 196
206 AHSSLLIGWF-----SHRPFVAAGVAV-EGKHYRRRGIDCGSRMCCROEFFVDRE 258
197 COELAVVPVFPVPGESHRPFVVOARLSDSRIRKRGLEDGRTNLCROQFFIDRL 256
259 IGMNDMIIOPEGYANMFTGQCPPLHVAAGPGLSASFHTAVNLKLANAA-ACTTGRSGCC 317
257 IGMNDMIITPTGYGNYGCGSPAYLAGVGSASSFHTAVNQYRMRLNPGTV--NSCC 314
318 VPTSRRLPLSLYYDRDSNIVKTDIDPMVVEACGCS 352
315 IPTKLSTMSMLYFDDENIVKRDVPMVVEECGCA 349

RESULT 15
US-08-459-214-33
Sequence 33, Application US/08459214
Patent No. 5716810
GENERAL INFORMATION:
APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,214
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/197792
FILING DATE: 17-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/958414
FILING DATE: 08-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744207
FILING DATE: 12-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/215466
FILING DATE: 05-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/906729
FILING DATE: 31-DEC-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/827710
FILING DATE: 07-FEB-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/783910
FILING DATE: 03-OCT-1985
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 297206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
TOPOLOGY: Linear
US-08-459-214-33

Query Match 29.5%, Score 546, DB 1, Length 349;
Best Local Similarity 35.8%, Pred. No. 7,1e-46;
Matches 120; Conservative 65; Mismatches 122; Indels 28; Gaps 9;

44 IDLAKSLIDKHLISORPLSPVSGALKTALORLR-GPRRE--TLEH----- 90
17 LEAVRHLNRLQMGKRPITHAVPKAMVTLAKRLHAGKYREDGRVEIPHLDGHASGCA 76
91 DOROEVEIISFADTDLSSINOTRLEFHSGRMASGMEVROTFRMFVQ-FPH---NAT 145
77 DQGERVSEIISFAETDGLASSRVRLYFISNGNQLFVVOASLMLYLKLLPYVLEKSR 136
146 QTMNIRVLYRPTDNLITLSQYVYVQVNASGYOLLGPEAOACSGOHLTLEVPESOV 205
137 RRVKRVYVQEPGHDGRDVEKRVDLKRSQWHTLPLEATQALFERGERRLNLDVQCDG 196
206 AHSSLLIGWF-----SHRPFVAAGVAV-EGKHYRRRGIDCGSRMCCROEFFVDRE 258
197 COELAVVPVFPVPGESHRPFVVOARLSDSRIRKRGLEDGRTNLCROQFFIDRL 256
259 IGMNDMIIOPEGYANMFTGQCPPLHVAAGPGLSASFHTAVNLKLANAA-ACTTGRSGCC 317
257 IGMNDMIITPTGYGNYGCGSPAYLAGVGSASSFHTAVNQYRMRLNPGTV--NSCC 314
318 VPTSRRLPLSLYYDRDSNIVKTDIDPMVVEACGCS 352
315 IPTKLSTMSMLYFDDENIVKRDVPMVVEECGCA 349

Search completed: October 12, 2002, 02:10:49
Job time : 16.5 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: October 12, 2002, 01:13:12 ; Search time 27 Seconds
(without alignments)
1252.720 Million cell updates/sec

Title: US-09-684-383-4

Perfect score: 1850
Sequence: 1 MASSLLALLFLPTTVVNP.....DSNIVKTIDPMVVEACGCS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database: PIR_71:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1850	100.0	352	2	JC5366
2	1844	99.7	352	2	S70580
3	1398	75.6	352	2	actin beta C pre
4	699.5	37.8	367	2	actin beta C cha
5	581.5	31.4	350	2	actin beta D cha
6	566.5	30.6	370	2	actin beta E cha
7	551	29.8	408	2	actin beta B sub
8	549.5	29.7	411	2	actin beta B cha
9	548.5	29.6	407	1	A40150
10	546	29.5	349	1	WEPGBA
11	543	29.4	424	1	WEPGBA
12	540	29.2	426	1	B24248
13	538	29.1	424	1	S31440
14	533.5	28.8	393	2	actin beta A cha
15	532.5	28.8	425	1	S50898
16	529.5	28.6	425	2	actin beta A cha
17	529	28.6	424	1	147072
18	528	28.5	413	2	actin beta A cha
19	456	24.6	255	2	actin beta B-1 c
20	356	19.2	115	2	actin beta B-2 c
21	350	19.1	115	2	actin beta A cha
22	350	19.1	115	2	actin beta A cha
23	312.5	16.9	101	2	actin beta A cha
24	311.5	16.8	101	2	actin beta A cha
25	292	15.8	102	2	actin beta A cha
26	283.5	15.3	373	2	actin beta A cha
27	273	14.8	396	1	actin beta A cha
28	261.5	14.1	393	2	actin beta A cha
29	257	13.9	394	2	actin beta A cha

30	252.5	13.6	372	2	C39364	GDF-1 embryonic gr
31	252.5	13.6	401	2	JH0689	bone morphogenetic
32	245.5	13.5	400	2	A49147	bone morphogenetic
33	249	13.5	357	2	A39364	GDF-1 embryonic gr
34	248	13.4	454	1	BH005	bone morphogenetic
35	246	13.3	402	2	A45056	bone morphogenetic
36	244.5	13.2	353	2	150607	bone morphogenetic
37	244.5	13.2	510	2	A54798	Vg-1-related prote
38	243.5	13.2	408	2	S58791	bone morphogenetic
39	243.5	13.2	513	1	BH005	bone morphogenetic
40	243	13.1	398	2	JH0688	bone morphogenetic
41	243	13.1	398	2	JH0687	bone morphogenetic
42	241.5	13.1	365	2	T43286	act-1 protein - ca
43	239	12.9	452	2	I49542	bone morphogenetic
44	238.5	12.9	313	2	I51284	bone morphogenetic
45	235.5	12.7	426	2	JH0690	bone morphogenetic

ALIGNMENTS

RESULT 1

JC5366
actin beta C - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 26-Aug-1999
C:Accession: JC5366
R:Fang, J.; Wang, S.; Smiley, E.; Bonadio, J.
Biochem. Biophys. Res. Commun. 231, 655-661, 1997
A:Title: Genes coding for mouse actin beta C and beta E are closely linked and exhl
A:Reference number: JC5366; M01D:97224404
A:Accession: JC5366
A:Molecule type: DNA
A:Residues: 1-352 <FAN>
A:Cross-references: GB:095962
C:Comment: Actin beta C and beta E form a distinct subset of related actins.
C:Genetics:
A:Introns: 105/3
C:Superfamily: Inhibin

Query Match 100.0%; Score 1850; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.6e-162;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	1	MASSLLALLFLPTTVVNPKEGCPACGAIPLDLSORELLDLAKSILDKLHLSOR	60
Db	1	MASSLLALLFLPTTVVNPKEGCPACGAIPLDLSORELLDLAKSILDKLHLSOR	60
Oy	61	PLSRPVSRGALKTRALQRLRPRRETLEHDOEOEYELISPADTDLSSINOTRLEFHS	120
Db	61	PLSRPVSRGALKTRALQRLRPRRETLEHDOEOEYELISPADTDLSSINOTRLEFHS	120
Oy	121	GMASGMEVROTRMEFVQFPFNATQTMNIRVLRDYDTNLITTSQYVQVNASQYOL	180
Db	121	GMASGMEVROTRMEFVQFPFNATQTMNIRVLRDYDTNLITTSQYVQVNASQYOL	180
Oy	181	LLGPPAQAACSGHITLLEVPESQVANSLLLGWFSRRPVAAOVREKGRHRRRGIDC	240
Db	181	LLGPPAQAACSGHITLLEVPESQVANSLLLGWFSRRPVAAOVREKGRHRRRGIDC	240
Oy	241	OGGSRMCCOEFEVDFPREIGNNDWIIOPEGYAMNFCGOCPLHVAAGPGISASPHAVLN	300
Db	241	OGGSRMCCOEFEVDFPREIGNNDWIIOPEGYAMNFCGOCPLHVAAGPGISASPHAVLN	300
Oy	301	LKANAAGTTGRGSCCVPTSRRLSLLYRDSNIVKTDIPDMVVEACGCS	352
Db	301	LKANAAGTTGRGSCCVPTSRRLSLLYRDSNIVKTDIPDMVVEACGCS	352

RESULT 2
S70580
actin beta C precursor - mouse
C:Species: Mus musculus (house mouse)

C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
 C/Accession: S70580
 R:Lau, A.L.; Nishimori, K.; Matzuk, M.M.
 Biochim. Biophys. Acta 1307, 145-148, 1996
 A>Title: Structural analysis of the mouse activin beta-C gene.
 A/Reference number: S70580; MUID:96283807
 A/Accession: S70580
 A>Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-352 <LAU>
 A/Cross-references: EMBL:U40772
 C/Genetics:
 A/Introns: 106/1
 C/Superfamily: Inhibin

Query Match 99.7% Score 1844; DB 2; Length 352;
 Best Local Similarity 99.7%; Pred. No. 2,7e-161;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 MASSLLALFLPTTYYNPKTEGPCACGALFDLESORELLDLAKSILDKLHSOR 60
Db 1 MASSLLALFLPTTYYNPKTEGPCACGALFDLESORELLDLAKSILDKLHSOR 60
OY 61 PILSPVSRGALKTALQRLRGPRRETLLEHDOOEYEIISFADTDLSSINOTRLEFHS 120
Db 61 PILSPVSRGALKTALQRLRGPRRETLLEHDOOEYEIISFADTDLSSINOTRLEFHS 120
OY 121 GRMASGHEVROTFRMFVOPPHNATOTMNIIRVLRPYDTNLTLSQYVVOYVNASGWOL 180
Db 121 GRMASGHEVROTFRMFVOPPHNATOTMNIIRVLRPYDTNLTLSQYVVOYVNASGWOL 180
OY 181 LLGPEAOACSGQHLTLELVESOVASHSLILGWFSHRPFVAOAVRVECKHVRRRGIDC 240
Db 181 LLGPEAOACSGQHLTLELVESOVASHSLILGWFSHRPFVAOAVRVECKHVRRRGIDC 240
OY 241 QGGRSMCCROEFFVDFREIGMNDWIIQPEGYAMNFCIGCCPLHVAGMPSISFHTAVL 300
Db 241 QGGRSMCCROEFFVDFREIGMNDWIIQPEGYAMNFCIGCCPLHVAGMPSISFHTAVL 300
OY 301 LLANMAAGTTGGSCCPTSRRLSLYYDRDSNIVTKDIPDMVVEACGCS 352
Db 301 LLANMAAGTTGGSCCPTSRRLSLYYDRDSNIVTKDIPDMVVEACGCS 352

```

RESULT 3

JC2466
 Inhibin beta-C chain precursor - human
 N/Alternate names: activin beta C chain
 C/Species: Homo sapiens (man)
 C/Date: 29-Mar-1995 #sequence_revision 26-May-1995 #text_change 29-Oct-1999
 C/Accession: JC2466
 R:Hoecton, G.; Neidhardt, H.; Schneider, C.; Pohl, J.
 Biochem. Biophys. Res. Commun. 206, 608-613, 1995
 A>Title: Cloning of a new member of the TGF-beta family: A putative new activin beta-C
 A/Reference number: JC2466; MUID:95126961
 A/Accession: JC2466
 A/Molecule type: mRNA
 A/Residues: 1-352 <HOE>
 A/Cross-references: GB:X82540; NID:9669154; PID:CA57890.1; PID:9669155
 A/Experimental source: Liver
 C/Genetics:
 A/Gene: GDB:INHBC
 A/Cross-references: GDB:632884
 A/Map position: 2cen-2q13
 C/Superfamily: Inhibin
 C/Keywords: glycoprotein
 F:1-18/Domain: signal sequence #status predicted <Sig>
 F:19-236/Domain: propeptide #status predicted <Pro>
 F:237-352/Product: activin beta C #status predicted <Mat>
 F:110,143,161/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.6% Score 1398; DB 2; Length 352;
 Best Local Similarity 76.2%; Pred. No. 2.3e-120;

Matches 269; Conservative 32; Mismatches 50; Indels 2; Gaps 2;

```

OY 1 MASSLLALFLPTTYYNPKTEGPCACGALFDLESORELLDLAKSILDKLHSOR 60
Db 1 MASSLLALFLPTTYYNPKTEGPCACGALFDLESORELLDLAKSILDKLHSOR 60
OY 61 PILSPVSRGALKTALQRLRGPRRETLLEHDOOEYEIISFADTDLSSINOTRLEFHS 120
Db 61 PILSPVSRGALKTALQRLRGPRRETLLEHDOOEYEIISFADTDLSSINOTRLEFHS 120
OY 121 GRMASGHEVROTFRMFVOPPHNATOTMNIIRVLRPYDTNLTLSQYVVOYVNASGWOL 180
Db 121 GRMASGHEVROTFRMFVOPPHNATOTMNIIRVLRPYDTNLTLSQYVVOYVNASGWOL 180
OY 181 LLGPEAOACSGQHLTLELVESOVASHSLILGWFSHRPFVAOAVRVECKHVRRRGIDC 240
Db 181 LLGPEAOACSGQHLTLELVESOVASHSLILGWFSHRPFVAOAVRVECKHVRRRGIDC 240
OY 241 QGGRSMCCROEFFVDFREIGMNDWIIQPEGYAMNFCIGCCPLHVAGMPSISFHTAVL 300
Db 241 QGGRSMCCROEFFVDFREIGMNDWIIQPEGYAMNFCIGCCPLHVAGMPSISFHTAVL 300
OY 301 LLANMAAGTTGGSCCPTSRRLSLYYDRDSNIVTKDIPDMVVEACGCS 352
Db 301 LLANMAAGTTGGSCCPTSRRLSLYYDRDSNIVTKDIPDMVVEACGCS 352

```

RESULT 4

JC4151
 Activin beta D chain precursor - African clawed frog
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
 C/Accession: JC4151
 R:Oda, S.; Nishimatsu, S.; Murakami, K.; Ueno, N.
 Biochem. Biophys. Res. Commun. 210, 581-588, 1995
 A>Title: Molecular cloning and functional analysis of a new activin beta subunit: a d
 A/Reference number: JC4151; MUID:95275314
 A/Accession: JC4151
 A/Molecule type: mRNA
 A/Residues: 1-367 <ODA>
 A/Cross-references: DDBJ:D49543; NID:9661512; PID:BA08494.1; PID:9661513
 A/Experimental source: embryo
 C/Superfamily: Inhibin
 C/Keywords: glycoprotein; mesoderm
 F:1-253/Domain: signal sequence #status predicted <Sig>
 F:254-367/Product: activin beta D chain #status predicted <Mat>
 F:64,155,161,208,230/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.8% Score 699.5; DB 2; Length 367;
 Best Local Similarity 39.3%; Pred. No. 3e-56;

```

OY 6 LALFLPTTYYNPKTEGPCACGALFDLESORELLDLAKSILDKLHSORPILSR 65
Db 6 LALFLPTTYYNPKTEGPCACGALFDLESORELLDLAKSILDKLHSORPILSR 65
OY 14 LLTLLGALAASQGLTKKSCPCG-----VQKEVIELAKOQIILKLERPITH 67
Db 14 LLTLLGALAASQGLTKKSCPCG-----VQKEVIELAKOQIILKLERPITH 67
OY 66 PVSRAKLTALQRLRGPRRETLLEHDOOEYEIISFADTDLSSINOTRLEFHS 113
Db 66 PVSRAKLTALQRLRGPRRETLLEHDOOEYEIISFADTDLSSINOTRLEFHS 113
OY 66 PVRGAVALNALRLHLNPRMELFGSMDNSNENTDTQOQSTIEISFETETVENS 127
Db 66 PVRGAVALNALRLHLNPRMELFGSMDNSNENTDTQOQSTIEISFETETVENS 127
OY 114 RLEHFGSRMASGHEVROTFRMFVOPPHNATOTMNIIRVLRPYDTNLTLSQYVVOYV 173
Db 114 RLEHFGSRMASGHEVROTFRMFVOPPHNATOTMNIIRVLRPYDTNLTLSQYVVOYV 173
OY 128 TLNFOFTDKDQSAHVLOAHMLLFFKANRTSQNETIRLVLYOAVSRRLISEKLE 187
Db 128 TLNFOFTDKDQSAHVLOAHMLLFFKANRTSQNETIRLVLYOAVSRRLISEKLE 187
OY 174 ASGWYQLLLGPEAOACSGQHLTLEL-----VPSOVASHSLILGWFSHRPFVAO 224
Db 174 ASGWYQLLLGPEAOACSGQHLTLEL-----VPSOVASHSLILGWFSHRPFVAO 224
OY 188 WTGNQTEFLAKSMIDTFPDGKNSLQLELNCDDGQDVPVLANPN-----SHQPLVAO 240
Db 188 WTGNQTEFLAKSMIDTFPDGKNSLQLELNCDDGQDVPVLANPN-----SHQPLVAO 240
OY 225 VRY-EGKHVRARRIDCOGGRSMCCROEFFVDFREIGMNDWIIQPEGYAMNFCIGCCPLH 283
Db 225 VRY-EGKHVRARRIDCOGGRSMCCROEFFVDFREIGMNDWIIQPEGYAMNFCIGCCPLH 283
OY 241 AKVHDSHATKRLSLNCDONSILCCRKYDYVDFKIDGMNDWIIKPGCYOINICMGKCPMH 300
Db 241 AKVHDSHATKRLSLNCDONSILCCRKYDYVDFKIDGMNDWIIKPGCYOINICMGKCPMH 300
OY 284 VAGMPGISASHTAVLNLANMAAGTTGGSCCPTSRRLSLYYDRDSNIVTKDIPD 343

```

DB 301 IAGAFGMAASHRTTVNLKANKNN--OTAVNSCCVPTKRRLPSLMDYDRNNVNLKTDIAD 358
 OY 344 MVEACGCS 352
 DB 359 MIVEACGCS 367

RESULT 5

activin beta E chain precursor - mouse
 JCS241
 C:Species: Mus musculus (house mouse)
 C:Date: 25-Apr-1997 #sequence_revision 09-May-1997 #text_change 29-Oct-1999
 C:Accession: JCS241; JCS367
 R:Yang, J.; Yin, W.; Smiley, E.; Wang, S.O.; Bonadio, J.
 Biochem. Biophys. Res. Commun. 228, 669-674, 1996
 A:Title: Molecular cloning of the mouse activin beta E subunit gene.
 A:Reference number: JCS241; MUID:97096313
 A:Contents: Liver
 A:Accession: JCS241
 A:Molecule type: mRNA
 A:Residues: 1-350 <FAN>
 A:Cross-references: GB:U96386; NID:92072521; PIDN:AAB53801.1; PID:92072522
 R:Yang, J.; Wang, S.; Smiley, E.; Bonadio, J.
 Biochem. Biophys. Res. Commun. 231, 655-661, 1997
 A:Title: Genes coding for mouse activin beta C and beta E are closely linked and exhibit
 A:Reference number: JCS366; MUID:97224404
 A:Accession: JCS367
 A:Molecule type: DNA
 A:Residues: 1-350 <FAA>
 A:Cross-references: GB:U96386; NID:92072521; PIDN:AAB53801.1; PID:92072522
 C:Genetics:
 A:Introns: 99/3
 C:Superfamily: Inhibin

Query Match 31.4%; Score 581.5; DB 2; Length 350;
 Best Local Similarity 37.7%; Pred. No. 1.9e-45;
 Matches 140; Conservative 66; Mismatches 110; Indels 55; Gaps 14;

OY 5 LLLALLFLPTTVNPKTEGPCACGAIFDLESQRELLDLAKKSIDKHLISQRPILS 64
 DB 12 LLMALVWV-----OSRSACPSGCGPTLADQGERALVLELAKOOLLEGHLISRPIT 64
 OY 65 RPYSGALKTALQRLRGPR-----RETLHNDQREVEIISFAD--TDLSTINQRL 116
 DB 65 RPLPOLALTRALRLQ--PKSMYGNRE-----KVISFATIIDKSTYRSMLT 111
 OY 117 FHSGRMASGMEYRQTFMEFVQFPHNATQMINIRVLYLRPYDTNL---TLTQYVVOV 172
 DB 112 FQSLPSLMSHL---YHARIMLHVPPSPFGTLYLR--IFRCGTRCGRGRTFLAHH--QT 163
 OY 173 MASGVOQLLGPDAQACSGHLLTEL-----VPESOVNHSLLIGWF--SHRPVNAVQ 225
 DB 164 TSSGMVHLTPSSGLNSEDSGVVKQLDLFRPLDLNSTAAGLPRLLDPTAGQGRPLELKI 223
 OY 226 RVE--GKHVRRRGIDCGGSRMCRCQREFFVDFREIGNMDITQEGYAMNPTQGCPLH 283
 DB 224 RANRPGGRRARRRTPCEPRTPLCCRDHYVDFQELGMDWILQEGVQLNVCSCGCPRH 283
 OY 284 VAGMPGISAFHTAVNLKANA--AAGTTGSGCCVPTSRRLSLIYDRDSNIVKIDI 341
 DB 284 LAGSPGTAASFHSAVSLKANNPWAGS---SCCVPTARRLSLIYLDHNGNVVKTIDV 339
 OY 342 PDMVVEACGCS 352
 DB 340 PDMVVEACGCS 350

RESULT 6

151199
 activin beta B subunit - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999

C:Accession: 151199
 R:Dohrmann, C.E.; Hemmelfr-Briyanlou, A.; Thomsen, G.H.; Fields, A.; Woolf, T.M.; Welt
 Dev. Biol. 157, 474-483, 1993

A:Title: Expression of activin mRNA during early development in Xenopus laevis.
 A:Reference number: 151199; MUID:93273083
 A:Accession: 151199
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-370 <DOH>
 A:Cross-references: GB:S61773; NID:9386027; PIDN:AAB26863.1; PID:9386028
 C:Superfamily: Inhibin

Query Match 30.6%; Score 566.5; DB 2; Length 370;
 Best Local Similarity 34.7%; Pred. No. 4.9e-44;
 Matches 130; Conservative 73; Mismatches 137; Indels 35; Gaps 12;

OY 5 LLLALLFLPTTVNPKTEGPCACGAIFDLESQRELLDLAKKSIDKHLISQRPILS 62
 DB 4 LLLPILLAGLARTCAPSPTEPGCPSCHP---PMEPE---MLEVKKRHLITLLHMODRPN 57
 OY 63 LSRPYSGALKTALQRLRGPR-----TLEHD-----QREVEIISFADTDL 108
 DB 58 ITHMVPRAAMVSALKKLKLANGKREDGNLEFDLDGHSILPPGHSTENSALITFAETDOV 117
 OY 109 SINQRLAEFHSGRMASGMEYRQTFMEFVQFPH--NATQMINIRVLYLRPYDTNLTLT 165
 DB 118 TMSRVLTSTIANEGNONLFFQSNLWLYLKLEVMOKSRRIKIKYFODAFNPKMNM 177
 OY 166 SQYVVOVNASGVIQOLLGPDAQACSG--HLLTELVEESQVNAHSSLL---GMSFHRP 219
 DB 178 VERKKVDIRSGWHTPEPLTEALQISLFEDEGERLNLLEVODGCGEYSLVPIVYDPEESH 237
 OY 220 FVAQAVR--EGKHVRRRGIDCGGSRMCRCQREFFVDFREIGNMDITQEGYAMNPTCG 278
 DB 238 FLVYHARLADNKHRIKRLKLEDCGHTNLCCROQFYIDRLGLMDWILAPAGYGNVCEG 297
 OY 279 QCELVHAGMPGISAFHTAVNLKANA--AGTTGSGCCVPTSRRLSLIYDRDSNIV 337
 DB 298 SCPAYLAGVGSASFHTAVNVOYRRLGRLNPGTV--NSCCIPTKLSTMSMLYFDDEXNIV 355
 OY 338 KTDIPDMVVEACGCS 352
 DB 356 KRDVPMNIVDECGCA 370

RESULT 7

550899
 betab inhibin precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
 C:Accession: S50899
 R:Thompson, D.A.; Cronin, C.N.; Martin, F.
 Eur. J. Biochem. 226, 751-764, 1994
 A:Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and bet
 A:Reference number: S50897; MUID:95112839
 A:Accession: S50899
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-408 <THO>
 A:Cross-references: EMBL:U16240
 C:Genetics:
 A:Introns: 151/1
 C:Superfamily: Inhibin

Query Match 29.8%; Score 551; DB 2; Length 408;
 Best Local Similarity 34.4%; Pred. No. 1.5e-42;
 Matches 125; Conservative 65; Mismatches 135; Indels 38; Gaps 10;

OY 22 TEGPCACGAIFDLESQREL-----LIDLAKKSIDKHLISQRPILSRPYSGALKT 75
 DB 52 SDQCTGSCG---FRRPELGRVDDGFLEAVKRIHLNRLQMRGRNITTHAVPKAANYTA 107

```

OY 76 LORLE-GRRE---TLEEH-----DOROEELTEIASADPLDSSINOTRLEPHHSGR 122
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 108 LRKLHAGVREDGRREIETHLGHASPGADGGERSEITISPAETDGLASSRVLFTLSNE 167
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 123 MASGHEVQOTRMEFPVQEPHNAOTQMNIRVLYLRPYDNTLTLSQVY----QVAVASGW 177
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 168 GNQNLFFVVAQASIMLYLTKLLPFLVLEKGGRRKRVKRYVQEGQPGDRAVAEVRDLKRSW 227
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 178 YOLLGPEPAQAACSGOHLTTELVEESQVAAHSSLIGMF-----SHRPFAAOVRV-EGK 230
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 228 HTFFLPTEPIQALFSGRGERRLSLDVQCCSCRELAVVPFVUPDGEESHRRPFAVARGDSR 287
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 231 HRVRRRGIDCGGSRMCCROEFPFDFREIGNDMTIOTPEGYAMNFCTGQCPLHVAAMPGI 290
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 288 HRIRKRGLECGGRNLCCRODFFIDFRLIGWNMDIAPTYGYNRYCEGSCPATLACVPGS 347
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 291 SASFTAVLNLNLKANA-ACTTGRGSCCVPTSRRLPLSLAYDSDSNIVKDIIDPMVENC 349
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 348 ASSFTAVVQNYRMRGLNPGTV--NSSCIPTKLTSMMLTFDDEYNIYKRDVFNMIIVEEC 405
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 350 GCS 352
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 406 GCA 408
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT &

Inhibin beta-B chain precursor - rat
 A:Alternate names: Inhibin/activin beta B-chain
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 03-Apr-1992 #sequence
 C:Accession: BA1398, I53288, C40905
 R:Feng, Z.M.; Li, Y.P.; Chen, C.L.C.
 Mol. Endocrinol. 3, 1914-1925, 1989
 A>Title: Analysis of the 5'-flanking regions of rat inhibin alpha- and beta-B-subunit genes
 A:Reference number: AA1398; MUID:90190649
 A:Accession: BA1398; MUID:90190649
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-174 <RES>
 A:Cross-references: GB:M32756; GB:M32757; NID:g204943; PIDN:AAA41438.1; PID:g554460
 R:dykema, J.C.; Mayo, K.E.
 Endocrinology 135, 702-711, 1994
 A>Title: Two messenger ribonucleic acids encoding the common beta B-chain of Inhibin and
 A:Reference number: I53288; MUID:94307180
 A:Accession: I53288
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-7 <RES>
 A:Cross-references: GB:S72477; NID:g619268
 R:Esch, F.S.; Shimazaki, S.; Cooksey, K.; Mercado, M.; Mason, A.J.; Ying, S.Y.; Ueno, N.
 Mol. Endocrinol. 1, 388-396, 1987
 A>Title: Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence analysis of
 A:Reference number: A40905; MUID:90331931
 A:Accession: C40905
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 133-411 <ESC>
 A:Superfamily: Inhibin

Query Match	29.7%	Score 549.5;	DB 2:	Length 411;
Best Local Similarity	32.8%	Pred. No. 2e-42;		
Matches 134;	Conservative 67;	Mismatches 142;	Indels 65;	Gaps 12

```

0Y 2 ASLLLLFL-----PPTVVPKRG-----CACGATIDLESOREL 42
    | | | | |
Db 12 ACULLLAAMGLPEAMGSPFPSPAPAPPPPPGAPGGSODTCTSCGGGGGFRRPBEL 71
    | | | | |
QY 43 -----LDLAKSLTDLMLHSQPLISRPYSKALKTALQRLR-GPRE--TLLH-- 90
    | | | | |
Db 72 GRVDGPFLEAVKRLISRLDLGRNRTTHVAPPAAMVTLRLKHLHGKREGEDEIPLD 131
    | | | | |
QY 91 -----DORGEYILISFADTLLSSINQRLREHFSGRMAEGMEYROTREWFVQ--FPH 142
    | | | | |

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Db      132 GHASPGADGQGVRSVLSIAFETDGLASSRRLKVFYFNSNEGONLLEFYVASLMLTKLLPY 191
Oy      143 -----NATOTNIRIVLRLRPYDTNLTLSOVYVQNASGWOLLILGPEAOAAGSOGHLTLE 198
Db      192 VLEKGRSRKRVKRVYFQEGEGHDDRNMYVEKKVYDLKSGCHMTPTTPIIDIALQALFERGERLN 251
Oy      199 LVPESOVAHSLILGTF-----SHRPVAAQVRV-BGKHVRVRGIDICGGSRMCCRDE 251
Db      252 LDVQCDSCQCELAIVLPFVDPGEESHRPVPVQAARLIDDSRRIRIKRGLCDBDSTSLCRQO 311
Oy      252 FEVDVERIGIMDWIITQEGYAMNCTQCQCLPAAHAGPGISAFSTHRAVNLTKAAVAAAGTT 311
Db      312 FFIDFRLIGIMDWIITAPGYGNYCCESCPAYLAGVGSASSFHTAVVNOYRM----- 364
Oy      312 GRG-----SCCVPTSRRLPTLILYRDNRINIKTDIIPMVAEAGCS 352
Db      365 -RGNGRPVNVSCCIPTKLSSMSMLTEDEENIVYKROVPNNVIEEGCA 411

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RESULT 5

Inhibin beta-B-chain precursor - human
 N: Alternate names: activin AB chain B
 C: Species: Homo sapiens (man)
 C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Dec-2000
 C: Accession: A40150; C24248; A40156; S10751
 R: Mison, A.J.; Berkemeier, L.M.; Schmelzer, C.H.; Schwall, R.H.
 M: Endocrinol. 3, 1352-1358, 1989
 A: Title: Activin B: precursor sequences, genomic structure and in vitro activities.
 A: Reference number: A40150; MUID:9014200
 A: Accession: A40150
 A: Molecule type: DNA
 A: Residues: 1-407 <MA>
 A: Cross-references: GB:M31668; GB:M31669; NID:g186419; PIDN:AAA59451.1; PID:g386827
 R: Mison, A.J.; Niall, H.D.; Seeburg, P.H.
 Blochem. Biophys. Res. Commun. 135, 957-964, 1986
 A: Title: Structure of two human ovarian inhibinls.
 A: Reference number: A90123; MUID:86186863
 A: Accession: C24248
 A: Molecule type: mRNA
 A: Residues: 55-407 <MA2>
 A: Cross-references: GB:M31437; NID:g186416; PIDN:AAA59169.1; PID:g186417
 R: Peng, Z.M.; Bardin, C.W.; Chen, C.L.C.
 Mol. Endocrinol. 3, 939-948, 1989
 A: Title: Characterization and regulation of testicular inhibin beta-subunit mRNA.
 A: Reference number: A40156; MUID:89295443
 A: Accession: A40156
 A: Molecule type: mRNA
 A: Residues: 22-46, 'A', 48-407 <FEN>
 A: Cross-references: GB:M31632
 A: Experimental source: testis
 R: Schmelzer, C.H.; Burton, L.E.; Tamony, C.M.; Schwall, R.H.; Mason, A.J.; Liegeois, P.
 Blochim. Biophys. Acta 1039, 135-141, 1990
 A: Title: Purification and characterization of recombinant human activin B.
 A: Reference number: S10751; MUID:90304183
 A: Accession: S10751
 A: Molecule type: protein
 A: Residues: 293-294, 'GX', 297-302, 'XX', 305-307 <SCH>
 C: Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respectively.
 C: Generation:

A:Gene: GDB:119347; OMIM:147390
A:Cross-references: GDB:119347; OMIM:147390
A:Map position: 2cen-2q13
C:Superfamily: inhibin
G:Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone
F:1-20/Domain: signal sequence #status predicted <SIC>
F:21-92/Domain: propeptide #status predicted <PRO>
F:93/Product: inhibin beta-chain #status predicted <MAT>
F:93/Binding site: carbohydrate (asn) (covalent) #status predicted

Best Local Similarity 33.3%. Pred. No. 2,5e-42;
Matches 134; Conservative 66; Mismatches 145; Indels 57; Gaps 13;

2 ASLLALFL-----PPTVANKTECP-----CPACGAIPLDLESREL 42
Db 12 ACLLLAACWLCPEAMGSPPTPTPAAPPPPPSPGSGDTCISCGG-----FRPREEL 67
43 -----LIDLAKSLIDLKLSORPLSRVSGALKTALQRLR-GPRRE---TLLEN-- 90
Db 68 GAVDDDFLEAVRHILSLQMGKRNITHAVPKAMVATLRKLGKVRDEGRVEIPLHD 127
49 1 -----DQROEYELISADTDLSSINOTRLEFHFSGMASGMEVROTREFPQ-FPH 142
Db 128 GHASPCADQOEVSSEIISPAETDGLASSRVRLYFISNEGONLFFVQASLWLYLKLTPY 187
143 ----NATOTMNRVLYLRDYDNLTLTSQVYVQVNASGYOLLPEAQAACSGHITLLE 198
Db 188 VLEKSRKRVKRVKVFQEOGHCHDRNNWKEKRVLDKRSCHMTPTLEATIALFERGERRLN 247
199 LVPESQVASHSLILGW-----SHRPVAAQVR-EGKHVRRRGIDCGGSRMCROE 251
Db 248 LDVQDCSCQELAVPVFVDPGESESHRPVAVQARLGDSSHRIRKRGLEDGRTNLCCROQ 307
252 FVDPREIGHNMWITQPEYAMNFCGCPPLHAGMPGISAFHTAVNLKANNA-AGT 310
Db 308 FIDRLIGMNMWITAPGYGYNCYEGSPAYLAVPGSASSFHTAVNOYRMGLNPGT 367
311 TCRGSCVPTSRPLSLYYDRDSNIVKTDIDPMVVEACGS 352
Db 368 V--NSCIPTRKSTMSMLYFDENYIVKRDVPMIIVECGCA 407

RESULT 10

WFGGB

Inhibin beta-B chain precursor - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 01-Dec-2000

C:Accession: A01394

R:Maeson, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Guillemin, R.

Nature 318, 659-663, 1985

A:Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precursor

A:Reference number: A93371; MUID:86092207

A:Accession: A01394

A:Molecule type: mRNA

A:Residues: 1-349 <MAS>

A:Cross-references: GB:X03267; NID:92005; PIDN:CAA27021.1; PID:92006

C:Comment: The source of this protein is ovarian follicular fluid.

C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide

C:Comment: Different forms of inhibin have been isolated (A and B) that differ in the amino-terminal

C:Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of follicle

C:Superfamily: Inhibin

C:Keywords: contraceptive; follitropin inhibitor; glycoprotein; gonad

F:1-334/Domain: propeptide (fragment) #status predicted <PRO>

F:235-349/Product: Inhibin beta-B chain #status predicted <MAS>

F:35/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.5%; Score 546; DB 1; Length 349;

Best Local Similarity 35.8%; Pred. No. 3.4e-42;

Matches 120; Conservative 65; Mismatches 122; Indels 28; Gaps 9;

44 LIDLAKSLIDLKLSORPLSRVSGALKTALQRLR-GPRRE---TLLEN----- 90
Db 17 LEAVRHILSLQMGKRNITHAVPKAMVATLRKLGKVRDEGRVEIPLHDGASPCA 76
49 91 DQROEYELISADTDLSSINOTRLEFHFSGMASGMEVROTREFPQ-FPH----NA 145
Db 77 DQROEYELISADTDLSSINOTRLEFHFSGMASGMEVROTREFPQ-FPH----NA 145
49 146 QTMNIRVLYLRDYDNLTLTSQVYVQVNASGYOLLPEAQAACSGHITLLEVPESOV 205
Db 137 RRVKRVKRVKRVKVFQEOGHCHDRNNWKEKRVLDKRSCHMTPTLEATIALFERGERRLNLDVQDCG 196
49 206 AHSLLILGW-----SHRPVAAQVR-EGKHVRRRGIDCGGSRMCROEFTVDFRE 258

Db 197 COELAVPVFVDPGESESHRPVAVQARLGDSSHRIRKRGLEDGRTNLCCROQFFIDRL 256

49 259 IGMNDWITQPEYAMNFCGCPPLHAGMPGISAFHTAVNLKANNA-AGTGRSGC 317

Db 257 IGMNDWITQPEYAMNFCGCPPLHAGMPGISAFHTAVNLKANNA-AGTGRSGC 317

49 318 VPTSRPLSLYYDRDSNIVKTDIDPMVVEACGS 352

Db 315 IPTKSTMSMLYFDENYIVKRDVPMIIVECGCA 349

RESULT 11

WFGGBA

Inhibin beta-A chain precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999

C:Accession: A01393

R:Maeson, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Guillemin, R.

Nature 318, 659-663, 1985

A:Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precurs

A:Reference number: A93371; MUID:86092207

A:Accession: A01393

A:Molecule type: mRNA

A:Residues: 1-424 <MAS>

A:Cross-references: GB:X03266; NID:92002; PIDN:CAA27020.1; PID:92003

C:Comment: The source of this protein is ovarian follicular fluid.

C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide

C:Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of fol

C:Superfamily: Inhibin

C:Keywords: contraceptive; follitropin inhibitor; glycoprotein; gonad

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-308/Domain: propeptide #status predicted <PRO>

F:309-424/Product: Inhibin beta-A chain #status predicted <MAS>

F:165/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.4%; Score 543; DB 1; Length 424;

Best Local Similarity 31.6%; Pred. No. 8.4e-42;

Matches 133; Conservative 67; Mismatches 141; Indels 80; Gaps 11;

6 LIALFLPTTVANKTEG-----PCPACGAIPLDLESRELIDLAKSLIDLKLS 58
Db 10 LILASCMWIVRSPPTSGSGHSAAPDCPCALATLPKDVPSQPMVEAVKKNILNMLLK 69
49 59 QPILSRVSGALKTALQRLR-----GPRRETLLENDQOEYELISF 102
Db 70 KRPDVTQVPRPAALNLNATRLKLVKGVENGVELEDDIGRAEM---NELMEQSEIITF 126
49 103 ADTDLSSINOTRLEFHFSGMASGMEVROTREFPQ-FPH-NATOT-MNIRVLY----- 153
Db 127 AEAGTA---KRTLREIISKESDLSYVERAELWFLKPKANRRRTKVSITLFPQOORPO 183
49 154 -----VLRDYDNLTLTSQVYVQVNASGYOLLPEAQAACSGHITLLEVP 202
Db 184 GSADAGEAEVDVGPPEEKSEVLISEKVVDAKSTMHIFPVSSIORLLDOKSALDIRTA 243
49 203 SQVAH-----SSILG-----WSPRPVAAQVR--VEGKH 231
Db 244 GECHETGASLVLLGKKKKKEEAEGKRKDEGAGVDEEKQSHRPPLMLQAROSEHPH 303
49 232 VRRRRGIDCGGSRMCROEFTVDFREIGMNDWITQPEYAMNFCGCPPLHAGMPGIS 291
Db 304 RRRRRGLEDGRTNLCCROQFFIDRL 256
49 292 ASFTAVNLKANNAAGTGRSGCVPPTSRPLSLYYDRDSNIVKTDIDPMVVEACGC 351
Db 364 LSFHSTVINYRMGHSFPAFLKSCCVPPTKLRPMISMLYDDGQIMIKKIDQNMIVECGC 423
49 352 S 352
Db 424 S 424

RESULT 12

B24248

Inhibin beta-A chain precursor [validated] - human

N:Alternate names: activin A; activin AB chain A; erythroid differentiation factor; meg

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 08-Dec-2000

C:Accession: S30488; B23556; B24248; A30884; S33351; P00010

R:Unimolto, K.; Honda, S.I.; Ueno, N.; Murakami, K.; Fukamizu, A.

DNA Seq. 2, 103-110, 1991

A:Title: Structure and sequence analysis of the human activin beta(A) subunit gene.

A:Reference number: S30488; MUID:92135888

A:Accession: S30488

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-426 <TRAN>

A:Cross-references: EMBL:X57578; NID:928351; PIDN:CAA0805.1; PID:9825621

A>Note: the authors translated the codon GAG for residue 53 as Gly and GAG for residue 5

R:Stewart, A.G.; Milborrow, H.M.; Rling, J.M.; Crowther, C.E.; Forage, R.G.

FEBS Lett. 206, 329-334, 1986

A:Title: Human inhibin genes. Genomic characterization and sequencing.

A:Reference number: A91366; MUID:87005283

A:Accession: B23556

A:Molecule type: DNA

A:Residues: 311-426 <STE>

A:Cross-references: GB:X04447; NID:933928; PIDN:CAA28041.1; PID:933929

R:Meson, A.J.; Niall, H.D.; Seeburg, P.H.

Biochem. Biophys. Res. Commun. 135, 957-964, 1986

A:Title: Structure of two human ovarian inhibins.

A:Reference number: A90123; MUID:86186863

A:Accession: B24248

A:Molecule type: mRNA

A:Residues: 1-426 <MAS>

A:Cross-references: GB:M13436; NID:9186414; PIDN:AAA59168.1; PID:9307069

R:Murata, M.; Eto, Y.; Shibata, H.; Sakai, M.; Muramatsu, M.

Proc. Natl. Acad. Sci. U.S.A. 85, 2434-2438, 1988

A:Title: Erythroid differentiation factor is encoded by the same mRNA as that of the inh

A:Reference number: A30884; MUID:88190086

A:Accession: A30884

A:Molecule type: mRNA

A:Residues: 1-426 <MUR>

A:Cross-references: GB:J03634; NID:9181946; PIDN:AAA35787.1; PID:9181947

R:Beig, H.; Walter, M.; Northmann, W.

submitted to the EMBL Data Library, April 1993

A:Description: Nucleotide sequence coding for the mature subunit beta(A) of human inhib

A:Reference number: S33351

A:Accession: S33351

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 311-376, 'AC', 380-426 <BER>

A:Cross-references: EMBL:X72498; NID:9297786; PIDN:CAA51163.1; PID:9755740

R:Fujimoto, K.; Kawakita, M.; Kato, K.; Yonemura, Y.; Masuda, T.; Matsuzaki, H.; Hirose,

Biochem. Biophys. Res. Commun. 174, 1163-1168, 1991

A:Title: Purification of megakaryocyte differentiation activity from a human fibrous his

A:Reference number: P00010; MUID:91144591

A:Accession: P00010

A:Status: preliminary

A:Molecule type: protein

A:Residues: 311-313, 'X', 315-320, 'XX', 323-328, 'X', 330-334 <FNU>

C:Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respecti

bly beta-A and beta-B, respectively.

C:Genetics:

A:Gene: GDB:INHBA

A:Cross-references: GDB:119346; OMIM:147290

A:Map position: 7p15-7p13

A:Intons: 129/3

C:Superfamily: Inhibin

C:Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone

F:1-28/Domain: signal sequence #status predicted <SIG>

F:29-310/Domain: propeptide #status predicted <PRO>

F:311-426/Product: inhibin beta A chain #status experimental <MAT>

F:165/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match , 29.28; Score 540; DB 1; Length 426;

Best Local Similarity 31.2%; Pred. No. 1.6e-41;

Matches 132; Conservative 70; Mismatches 139; Indels 82; Gaps 11;

6 LLLALLFTPTTVVNPKEG-----PCPACGALF--DLRSORLLDLAKKSLIDKLHS 58

10 LLSASCTIVASPTPSGEGSAPDCPSALALPBDVRSQPEVAVKHTLNLHLK 69

59 QPRLSPVSRGALKTALORL-----GPRRTLLHIDROEEYIEIF 102

70 KRDPVQPVKALALNAIRKLHVKGNGYVEIEDDIGRAEM--NELMEQTSIEIF 126

103 ADPDLSSINGTLEPHFSGMAGMEVROTRFEPQPH-NATOR-AMIRVLYLRPY-- 158

127 AE--SGTARKTLHFEISLEGSDLSVEREVLFLKVPKANTFRKVTIRLEQQKHQ 183

159 -----DTNLTSTGYVVGWVAGSWQLLGPAPAAQSGCHLTLEL--- 199

184 GSLDTGEAEVGLKGBSELSEKVDARKSTWIVFVSSITQLDLDOGSSLDVRIA 243

200 VPESQVHSSLL-----GWFSHRPVAAQVR--VEG 229

244 CEQCESGASLVLLGKKKKKEEGEGKGGGAGAGADEKQSHRPFLMLQARQSEDH 303

230 KHRVRRRIGDCCGSRMCQREFFVDFRIGMDWLIQPGYAMNCTCCPLHVAQMG 289

304 PHRRRRRGLECDGKVNICKKQFFVSKDIGMDWIIARSCYHANYCEGECPSHIGTSG 363

290 ISASFRAVILNLKANAAGTTGSCVPTSRPSTLLIYDSDNIYVTDIIPDVVEAC 349

364 SLSFSTVYINHYRMGRSHFANLKSQCVPTKLRPSMLTYDDGQNIKKDIONMIVEEC 423

350 GCS 352

424 GCS 426

RESULT 13

S31440

Inhibin beta-A chain - mouse

N:Alternate names: activin A; mesoderm-inducing factor WEHI-MIF

C:Species: Mus musculus (house mouse)

C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 10-Sep-1999

C:Accession: A60087; I48265; S31440

R:Albano, R.M.; Goddave, S.F.; Huybregts, D.; Van Nijmen, K.; Isaacs, H.V.; Slack,

Development 110, 435-443, 1990

A:Title: A mesoderm-inducing factor produced by WEHI-3 murine myelomonocytic leukemia

A:Reference number: A60087; MUID:92155098

A:Accession: A60087

A:Molecule type: protein

A:Residues: 309-311, 'X', 313-318, 'XX', 321-325 <AL2>

R:Albano, R.M.; Groome, N.; Smith, J.C.

Development 117, 711-723, 1993

A:Title: Activins are expressed in preimplantation mouse embryos and in ES and EC cel

A:Reference number: I48243; MUID:93521614

A:Accession: I48265

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-424 <RES>

A:Cross-references: EMBL:X69619; NID:950145; PIDN:CAA49325.1; PID:950146

C:Superfamily: Inhibin

Query Match 29.1%; Score 538; DB 1; Length 424;

Best Local Similarity 32.1%; Pred. No. 2.4e-41;

Matches 136; Conservative 68; Mismatches 134; Indels 86; Gaps 14;

6 LLLALLFTPTTVVNPKEG-----PCPACGALFIDL-----ESQRELLDLAKKSLIDKL 55

10 LLSASCTIVASPTPSGEGSAPDCPSALALPBDVRSQPEVAVKHTLNLHLK 66

56 HLSORPLSPVSRGALKTALORL-----GPRRTLLHIDROEEYIEIF 99

67 HLKRPDVQPVKALALNAIRKLHVKGNGYVEIEDDIGRAEM--NELMEQTSIEI 123

Query Match 28.8% Score 533.5 DB 2 Length 393:
Best Local Similarity 32.0% Pred. No. 5.6e-41:
Matches 124: Conservative 83; Mismatches 139; Indels 41; Gaps 13:

1 MASSLLALFLTPPTVVNPKT---EGPCPAC-WGAIPLDESQRELLDLAKSLDKLH 56
13 LSVTCLMACTLLVOCSSLSGAETGSOESCSCGLHQEDSGMDQDFLAIVKRLHLRLQ 72
57 LSORPLSRPVSRGALKTALQLRLG-----PRRETLLEHQOEE-YETISFAD 104
73 MNERPITHPIPKAAVVTALRLKLGKVRDEGRVEIPLNDGHAHNEVEGETSEISFAE 132
105 TDLSTLNQRLRLEPHSGRNASGHEVQTR-FMEFVQFPINATQTNIRLY-LRPTQNL 162
133 SDVVPKSKSLFLISNEGONMLYVLOANLMLYFKLMPCTLEKGRAKVTAVHVSIEPG- 191
163 TLTSGVY-----VQVNASGMYOQLLCPRAQAACSOGLHLLELVPESQVHSSJLIGM 214
192 ---GQNVHMPMEKRRELRLRSGMHTFPVSEAIRMLAKGRMODLDIHCEGDEANVLEPI 248
215 F-----SHRPFAAQR-VREGKHVRVRRGIDOCGS-EMCCROEFVDFREIGNDWIT 266
249 LVDPSPDSNRPLVRAQAQADGKHKRIRKRGLEDGNNGLCCROQYIDFRLLGNMDWIT 308
267 OPEGVAMNCTGOCPLHVAGMEGISAFHTAVNLILKANA-AAAGTTGRCSCCVPTSRRLP 325
309 APAGYGYNCCEGSCPAYMAGVGPSSAFHTAVNQYRMRMGSPGSV--NSCICPTKLSTM 366
326 SLIYTRDSDNIYKTDIPDMVVEACGS 352

Query Match 28.8% Score 533.5 DB 2 Length 393:
Best Local Similarity 32.0% Pred. No. 5.6e-41:
Matches 124: Conservative 83; Mismatches 139; Indels 41; Gaps 13:

1 MASSLLALFLTPPTVVNPKT---EGPCPAC-WGAIPLDESQRELLDLAKSLDKLH 56
13 LSVTCLMACTLLVOCSSLSGAETGSOESCSCGLHQEDSGMDQDFLAIVKRLHLRLQ 72
57 LSORPLSRPVSRGALKTALQLRLG-----PRRETLLEHQOEE-YETISFAD 104
73 MNERPITHPIPKAAVVTALRLKLGKVRDEGRVEIPLNDGHAHNEVEGETSEISFAE 132
105 TDLSTLNQRLRLEPHSGRNASGHEVQTR-FMEFVQFPINATQTNIRLY-LRPTQNL 162
133 SDVVPKSKSLFLISNEGONMLYVLOANLMLYFKLMPCTLEKGRAKVTAVHVSIEPG- 191
163 TLTSGVY-----VQVNASGMYOQLLCPRAQAACSOGLHLLELVPESQVHSSJLIGM 214
192 ---GQNVHMPMEKRRELRLRSGMHTFPVSEAIRMLAKGRMODLDIHCEGDEANVLEPI 248
215 F-----SHRPFAAQR-VREGKHVRVRRGIDOCGS-EMCCROEFVDFREIGNDWIT 266
249 LVDPSPDSNRPLVRAQAQADGKHKRIRKRGLEDGNNGLCCROQYIDFRLLGNMDWIT 308
267 OPEGVAMNCTGOCPLHVAGMEGISAFHTAVNLILKANA-AAAGTTGRCSCCVPTSRRLP 325
309 APAGYGYNCCEGSCPAYMAGVGPSSAFHTAVNQYRMRMGSPGSV--NSCICPTKLSTM 366
326 SLIYTRDSDNIYKTDIPDMVVEACGS 352

```

Db          367      SMLYFDDEYNIVKRDVPMNVIIECCGA   393
|||||: |||| |:::|| |||:
RESULT 15
Inhibin beta-A chain precursor - bovine
S50898
N:Alternate names: activin; mesoderm inducing factor
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R:Accession: S50898; B25732; A60960; B61548
R:Thompson, D.A.; Cronin, C.N.; Martin, F.
Eur. J. Biochem. 226, 751-764, 1994
A>Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and bet
y DNase I footprinting.
A:Reference number: S50897; MUID:95112839
A:Accession: S50898
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-425 <TRH>
A:Cross-references: EMBL:U16238
R:Forage, R.G.; Ring, J.M.; Brown, R.W.; McInerney, B.V.; Cobon, G.S.; Gregson, R.P.;
Proc. Natl. Acad. Sci. U.S.A. 83, 3091-3095, 1986
A>Title: Cloning and sequence analysis of cDNA species coding for the two subunits oB
A:Reference number: A94097; MUID:86205842
A:Accession: B25732
A:Molecule type: mRNA
A:Residues: 258-423 <FOR>
A:Cross-references: GB:M13274; MID:g163196; PIDN:AAA97415.1; PID:g163197
A>Note: part of this sequence, including the amino end of the mature protein, was con
R:Chertov, O.Y.; Krasnosel'skii, A.L.; Bogdanov, M.E.; Hoperakaya, O.A.
Biomed. Sci. 1, 499-506, 1990
A>Title: Mesoderm-inducing factor from bovine amniotic fluid: purification and N-term
A:Reference number: A60960; MUID:92126853
A:Accession: A60960
A:Molecule type: protein
A:Residues: 310-312, 'X', 314-319, 'XX', 322-328, 'P' <CHE>
R:Fukuda, M.; Miyamoto, K.; Hasegawa, Y.; Nomura, M.; Igarashi, M.; Kangawa, K.; Mats
Mol. Cell. Endocrinol. 44, 55-60, 1986
A>Title: Isolation of bovine follicular fluid inhibin of about 32 kDa.
A:Reference number: A61548; MUID:86136989
A:Accession: B61548
A:Molecule type: protein
A:Residues: 310-313 <PUK>
C:Genetics:
A:Insertions: 130/1
C:Superfamily: Inhibin
C:Keywords: disulfide bond; glycoprotein; gonad; heterodimer; homodimer; hormone
F.1-28/Domain: signal sequence #status predicted <SIG>
F.29-309/Domain: propeptide #status predicted <PRO>
F.310-423/Product: beta-A inhibin/activin #status experimental <MAT>
F.165/Binding site: carbohydrate (asn) (covalent) #status predicted
Query Match                28.8%; Score 532.5; DB 1; Length 425;
Best Local Similarity     31.0%; Pred. No. 7.7e+41;
Matches 131; Conservative 70; Mismatches 140; Indels 81; Gaps 11:
Db          184      GSUDGAEAEVGGLGGESEMLISEKVVDARKSTWHIFPVSSCIORLLDQCKSSIDIRIA   243
|||||: |||| |:::|| |||:

```

```
Oy 200 VPESQVANSLLI-----GMFSHRPEVAAQVR--VEGK 230
Db 244 CEQCOETGASLVLLGKKKKKEEGEGKKRDEGCGAGDEKEKQSHRPFLMLQARQSEDP 303
Oy 231 HRRRRGIDCGGSRMCCRQEFVDFREIGNNDWITQPEGYAMNFCGQCPPLHVAQMPGI 290
Db 304 HRRRRGLECDGKVNICKKQFVDFKIDGNNDWITAPSGYHANYCEGECPSHIAGTSGS 363
Oy 291 SASFTAVLNLKANAAAGTGRGSCCVPTSRRLPLSLLYDRDSNIVKTDIPDMVVEACG 350
Db 364 SLSFHSYVNHRYMRGHSFPANLKSQCVPTKLRPSMLLYDDGQNTIKKDIONMIVECG 423
Oy 351 CS 352
Db 424 CS 425
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Search completed: October 12, 2002, 02:09:56
Job time : 28 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 22:35:53 ; Search time 13.5 seconds
(without alignments)

1009.576 Million cell updates/sec

Title: US-09-684-383-4

Perfect score: 1850
Sequence: 1 MASSILLALLFLPTTVNP.....DSNVKTDIDPMVEACGCS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1844	99.7	352	1	IHBC_MOUSE
2	1621.5	87.6	351	1	IHBC_RAT
3	1398	75.6	352	1	IHBC_HUMAN
4	594	32.1	350	1	IHBE_HUMAN
5	589.5	31.9	350	1	IHBE_RAT
6	581.5	31.4	350	1	IHBE_MOUSE
7	556	30.1	391	1	IHBB_CHICK
8	551	29.8	408	1	IHBB_BOVIN
9	548.5	29.6	407	1	IHBB_HUMAN
10	546	29.5	349	1	IHBB_PIG
11	543	29.4	424	1	IHBA_PIG
12	540	29.2	426	1	IHBA_HUMAN
13	538	29.1	424	1	IHBA_MOUSE
14	538	29.1	424	1	IHBA_RAT
15	534	28.9	426	1	IHBA_HORSE
16	532.5	28.8	425	1	IHBA_BOVIN
17	529.5	28.6	425	1	IHBA_SHEEP
18	494	26.7	424	1	IHBA_CHICK
19	456	24.6	255	1	IHBB_MOUSE
20	320	17.3	407	1	GDFF_HUMAN
21	316	17.1	405	1	GDFF_MOUSE
22	296	16.0	374	1	GDFF_BRAKE
23	295	15.9	375	1	GDFF_SHEEP
24	290	15.7	375	1	GDFF_HUMAN
25	289	15.6	375	1	GDFF_MOUSE
26	288	15.6	375	1	GDFF_PAPIA
27	288	15.6	375	1	GDFF_PIG
28	287	15.6	376	1	GDFF_RAT
29	283	15.3	375	1	GDFF_BOVIN
30	283	15.3	375	1	GDFF_MELGA
31	282	15.2	375	1	GDFF_CHICK
32	273	14.8	396	1	BMP2_HUMAN
33	272	14.7	345	1	GDFF_RAT

34	263.5	14.2	395	1	BMP2_RABIT
35	261.5	14.1	393	1	BMP2_RAT
36	260.5	14.1	396	1	BMP2_DAMDA
37	257	13.9	394	1	BMP2_MOUSE
38	252.5	13.6	372	1	GDFF_HUMAN
39	252.5	13.6	401	1	BMP4_XENTIA
40	249	13.5	357	1	GDFF_MOUSE
41	248	13.4	454	1	BMP5_HUMAN
42	246	13.3	402	1	BMP8_HUMAN
43	244.5	13.2	353	1	BMP2_CHICK
44	244.5	13.2	510	1	BMP6_MOUSE
45	243.5	13.2	408	1	BMP4_DAMDA

046564	Oryctolagus
P49001	rattus norv
O19006	dama dama
P21274	mus musculu
P27539	homo sapien
P30885	xenopus lae
P20863	mus musculu
P22003	homo sapien
P34820	homo sapien
O90751	gallus gall
P20722	mus musculu
O29607	dama dama

RESULT 1	
IHBC_MOUSE	STANDARD: PRT: 352 AA.
ID	P5104; 061452;
AC	01-OCT-1996 (Rel. 34, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Inhibin beta C chain precursor (Activin beta-C chain).
GN	IHBC.
OS	mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=129; TISSUE=Liver;
RX	MEDLINE=96435913; PubMed=8383799;
RA	Schmitt J., Hoellen G., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RA	Pohl J., Schrewe H.,
RT	Structure, chromosomal localization, and expression analysis of the
RT	mouse inhibin/activin beta C (inhbc) gene.;
RL	Genomics 32:358-366(1996).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96283807; PubMed=8679697;
RA	Lau A.L., Nishimori K., Matzuk M.M.;
RT	Structural analysis of the mouse activin beta C gene.;
RL	Biochim. Biophys. Acta 1307:145-148(1996).
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=97224404; PubMed=9070865;
RA	Fang J., Wang S.Q., Sallley E., Bonadio J.;
RT	Genes coding for mouse activin beta C and beta E are closely linked
RT	and exhibit a liver-specific expression pattern in adult tissues.;
RL	Biochem. Biophys. Res. Commun. 231:655-661(1997).
CC	-1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
CC	RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC	INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC	FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC	GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC	EMBRYOID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC	EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC	SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC	ACTIVINS.
CC	-1- SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH
CC	ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC	INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.
CC	ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY
CC	SIMILARITY).
CC	-1- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE ADULT LIVER.
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC	-----
CC	This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way

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DR EMBL: X90841: CA62347.1: JOINED.
 DR EMBL: X90842: CA62347.1: JOINED.
 DR EMBL: X90819: CA62333.1: JOINED.
 DR EMBL: U40773: AAC52723.1: JOINED.
 DR EMBL: U40772: AAC52723.1: JOINED.
 DR EMBL: U95962: AAC53164.1: JOINED.
 DR HSSP: P18075: 1BMP.
 DR MGP: MGI105932: 1mbc.
 DR InterPro: IPR002400: GF-cysknoc.
 DR InterPro: IPR001318: Inhibin_betaC.
 DR InterPro: IPR001839: TGF-beta.
 DR Pfam: PF00019: TGF-beta.1.
 DR PRINTS: PR00438: GRCYSKNOT.
 DR PRINTS: PR00672: INHIBINBC.
 DR PRODOM: PD000357: TGF-beta.1.
 DR SMART: SM00204: TGF-beta.1.
 DR PROSITE: PS00250: TGF-BETA.1.
 DR Growth factor: Hormone: Glycoprotein: Signal.
 KW SIGNAL 1 18
 FT PROPEP 19 236
 FT CHAIN 237 352
 FT DISULFID 240 248
 FT DISULFID 247 317
 FT DISULFID 276 349
 FT DISULFID 280 351
 FT DISULFID 316 316
 FT CARBOHYD 111 111
 FT CARBOHYD 143 143
 FT CARBOHYD 161 161
 FT CARBOHYD 173 173
 FT CONFLICT 243 243
 SQ SEQUENCE 352 AA: 39401 MW: 220812PD73717185 CRC64:
 Query Match 99.7% Score 1844: DB 1: Length 352:
 Best Local Similarity 99.7% Pred. No. 4.8e-164:
 Matches 351: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

QY 1 MASSLLALLFLPTTVNPKTEGPCACGAIPLDESORELLDLAKKSLDKLHLSOR 60
 DB 1 MASSLLALLFLPTTVNPKTEGPCACGAIPLDESORELLDLAKKSLDKLHLSOR 60
 QY 61 PILSRPVSGALKTALORLGRPRRETLLEHDOREYEELISFADTDLSSINOTRLEPHFS 120
 DB 61 PILSRPVSGALKTALORLGRPRRETLLEHDOREYEELISFADTDLSSINOTRLEPHFS 120
 QY 121 GRMASGMEVQTRFMFVQRPNNATOTMNRVLYRPTDNLTLTSQYVQVNAAGCYOL 180
 DB 121 GRMASGMEVQTRFMFVQRPNNATOTMNRVLYRPTDNLTLTSQYVQVNAAGCYOL 180
 QY 181 LAGPEAQAACSGHLLTELPEPESVAHSSILGWFSHRPVAAOVRECKHRYRRGIDC 240
 DB 181 LAGPEAQAACSGHLLTELPEPESVAHSSILGWFSHRPVAAOVRECKHRYRRGIDC 240
 QY 241 QGGSRMCCROEEFVDFEIGEMNDMIIOPEGYAMNFCGQCPPLHVAGMPGISAFHTAVLN 300
 DB 241 QGGSRMCCROEEFVDFEIGEMNDMIIOPEGYAMNFCGQCPPLHVAGMPGISAFHTAVLN 300
 QY 241 QGASRMCCROEEFVDFEIGEMNDMIIOPEGYAMNFCGQCPPLHVAGMPGISAFHTAVLN 300
 DB 241 QGASRMCCROEEFVDFEIGEMNDMIIOPEGYAMNFCGQCPPLHVAGMPGISAFHTAVLN 300
 QY 301 LKANAAGTGTGSCCVPTSRRLPLSLYYDRDSNIYKTDIPMAYEAGCCS 352
 DB 301 LKANAAGTGTGSCCVPTSRRLPLSLYYDRDSNIYKTDIPMAYEAGCCS 352

RESULT 2
 ID INBC_RAT STANDARD: PRT: 351 AA.
 AC Q9WUR5:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Inhibin beta C chain precursor (Activin beta-C chain).
 GN INHBC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar;
 RA Rossmann W., Peter B., Schulte-Hermann R.;
 RT "Rat activin beta C and beta E: sequence and expression."
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
 CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
 CC ACTIVINS.
 CC -1- SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH
 CC ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.
 CC ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY
 CC SIMILARITY). BELONGS TO THE TGF-BETA FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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DR EMBL: AF140031: AAD30132.1: -
 DR HSSP: P18075: 1BMP.
 DR InterPro: IPR002405: Inhibin_alpha.
 DR InterPro: IPR001318: Inhibin_betaC.
 DR InterPro: IPR001839: TGF-beta.
 DR Pfam: PF00019: TGF-beta.1.
 DR PRINTS: PR00669: INHIBINA.
 DR PRINTS: PR00672: INHIBINBC.
 DR PRODOM: PD000357: TGF-beta.1.
 DR SMART: SM00204: TGF-beta.1.
 DR PROSITE: PS00250: TGF-BETA.1.
 KW Growth factor: Hormone: Glycoprotein: Signal.
 KW SIGNAL 1 18
 FT PROPEP 19 236
 FT CHAIN 237 351
 FT DISULFID 239 246
 FT DISULFID 246 316
 FT DISULFID 275 348
 FT DISULFID 279 350
 FT DISULFID 315 315
 FT CARBOHYD 110 110
 FT CARBOHYD 142 142
 FT CARBOHYD 160 160
 SQ SEQUENCE 351 AA: 39335 MW: 68219BF6C3E180A1 CRC64:
 Query Match 87.6% Score 1621.5: DB 1: Length 351:
 Best Local Similarity 89.5% Pred. No. 2.4e-143:
 Matches 315: Conservative 11: Mismatches 25: Indels 1: Gaps 1:

QY 1 MASSLLALLFLPTTVNPKTEGPCACGAIPLDESORELLDLAKKSLDKLHLSOR 60
 DB 1 MASSLLALLFLPTTVNPKTEGPCACGAIPLDESORELLDLAKKSLDKLHLSOR 60
 QY 61 PILSRPVSGALKTALORLGRPRRETLLEHDOREYEELISFADTDLSSINOTRLEPHFS 120
 DB 61 PILSRPVSGALKTALORLGRPRRETLLEHDOREYEELISFADTDLSSINOTRLEPHFS 120

QY 121 GRMASGEVROTRFMFEVQFPHNATQTNIRVLYLRPYDTNLTLTSQYVVOVNASGYOL 180
 DB 120 DRTGGEVLYQTRFMFEVQFPHNATQTNIRVLYLRPYDTNLTLTSQYVVOVNASGYOL 179
 QY 181 LCPPEAQAACSGCHLTLELVPESSQVAHSSLLIGMFSHRPFAVAOVRGKRRVRRGIDC 240
 DB 180 LCPPEAQAACSGCHLTLELVPESSQVAHSSLLIGMFSHRPFAVAOVRGKRRVRRGIDC 239
 QY 241 CGGSRMCCROEFFVDPREIGMNDWIIOPGYAMNCTGOCPLHVAAGMGTISAFHTAVLN 300
 DB 240 CGGSRMCCROEFFVDPREIGMNDWIIOPGYAMNCTGOCPLHVAAGMGTISAFHTAVLN 299
 QY 301 LKANAAGTTGRCSCCVPTRSRPLSLLYDRDSNIVKTDIPDMVVEACGCS 352
 DB 300 LKANAAGTTGRCSCCVPTRSRPLSLLYDRDSNIVKTDIPDMVVEACGCS 351
 RESULT 3
 ID HIBC_HUMAN STANDARD: PRT: 352 AA.
 AC P5103:
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Inhibin beta C chain precursor (Activin beta-C chain).
 GN INHBC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=95126961; PubMed=7826378;
 RA Hechten G., Neidhardt H., Schneider C., Pohl J.;
 RT "Cloning of a new member of the TGF-beta family: a putative new
 RT activin beta C chain."
 RL Biochem. Biophys. Res. Commun. 206:608-613(1995).
 RL 121
 RP TISSUE SPECIFICITY.
 RX MEDLINE=98089987; PubMed=9428386;
 RA Thomas T.Z., Chapman S.M., Hong W., Gursingfhe C., Mellor S.L.,
 RA Fletcher R., Pedersen J., Risbridger G.P.;
 RT "Inhibins, activins, and follistatins: expression of mRNAs and
 RT cellular localization in tissues from men with benign prostatic
 RT hyperplasia."
 RL Prostate 34:34-43(1998).
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, NERVE CELL SURVIVAL,
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
 CC ACTIVINS.
 CC -1- SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH
 CC ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.
 CC ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY
 CC SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BENIGN PROSTATIC HYPERPLASIA.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC or send an email to license@isb-slb.ch).
 CC -----
 CC EMBL: X82540; CAA57890.1; -.

DR HSSP: P18075; 1BMP.
 DR MIM: 601233;
 DR InterPro: IPR002400; GF_cysknct.
 DR InterPro: IPR001318; Inhibin_betaC.
 DR InterPro: IPR001839; TGF-beta.
 DR Pfam: PF00019; TGF-beta.1.
 DR PRINTS: PR00458; GFCSKNCT.
 DR PRODOM: PD000357; TGF-beta.1.
 DR SMART: SM00204; TGF-beta.1.
 DR PROSITE: PS00250; TGF-BETA_1.
 KW Growth factor; Hormone; Glycoprotein; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 236
 FT CHAIN 237 352
 FT DISULFID 240 248
 FT DISULFID 247 317
 FT DISULFID 276 349
 FT DISULFID 280 351
 FT CARBOHYD 316 316
 FT CARBOHYD 110 110
 FT CARBOHYD 143 143
 FT CARBOHYD 161 161
 FT SEQUENCE 352 AA; 38238 MW; 496476AD82562D3E CRC64;
 SQ
 Query Match 75.6%; Score 1398; DB 1; Length 352;
 Best Local Similarity 76.2%; Pred. No. 1.5e-122;
 Matches 269; Conservative 32; Mismatches 50; Indels 2; Gaps 2;
 QY 1 MASSLLALLFLPTTVVNPKEGPCPCAGCAIFDESRELLDLAKSLDKLHLR 60
 DB 1 MTSLLLAFLFLPTTVVNPKEGPCPCAGCAIFDESRELLDLAKSLDKLHLR 60
 QY 61 PLSRPVSRGALKTALORLGRPRETLLEHDOREVEYLISPADTSLISNOTRLEPHFS 120
 DB 61 PTLNRPVSRALKTALORLGRPRETLLEHDOREVEYLISPADTSLISNOTRLEPHFS 119
 QY 121 GRMASGEVROTRFMFEVQFPHNATQTNIRVLYLRPYDTNLTLTSQYVVOVNASGYOL 179
 DB 120 SDRTAGREYQQAQLMFVQPLSNITWTLKRVLYLGPANTMLTATQYLLLEVDASGWHQ 179
 QY 180 LCPPEAQAACSGCHLTLELVPESSQVAHSSLLIGMFSHRPFAVAOVRGKRRVRRGIDC 239
 DB 180 LCPPEAQAACSGCHLTLELVPESSQVAHSSLLIGMFSHRPFAVAOVRGKRRVRRGIDC 239
 QY 240 CGGSRMCCROEFFVDPREIGMNDWIIOPGYAMNCTGOCPLHVAAGMGTISAFHTAVLN 300
 DB 240 CGGSRMCCROEFFVDPREIGMNDWIIOPGYAMNCTGOCPLHVAAGMGTISAFHTAVLN 299
 QY 300 LKANAAGTTGRCSCCVPTRSRPLSLLYDRDSNIVKTDIPDMVVEACGCS 352
 DB 300 LKANAAGTTGRCSCCVPTRSRPLSLLYDRDSNIVKTDIPDMVVEACGCS 352
 RESULT 4
 ID HIBC_HUMAN STANDARD: PRT: 350 AA.
 AC P58166;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibin beta E chain precursor (Activin beta-E chain).
 GN INHBE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Rhabdomyosarcoma;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.

FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 160 161 EH -> DY (IN REF. 2).
 SO SEQUENCE 350 AA: 38898 MW: 0CEBFE108E926E3 CRC64;
 Query Match 31.9%; Score 589.5; DB 1; Length 350;
 Best Local Similarity 39.2%; Pred. No. 2.4e-47;
 Matches 144; Conservative 54; Mismatches 122; Indels 47; Gaps 12;
 5 LLLALLFLPTTVVNPKEGCPACGAIFFDESQRELLDLAKSLDKLHLSQRPILS 64
 12 LLMALVWV-----QSTRSACPSGCGPTLAPQGERALVLELAKQILEGLHLSRPRT 64
 65 RYVSGALKTALQRLGRPR-----RETLLEHDQROEEYEIISFADTSSINQRLERH 118
 65 RPLPQALTRALRLQ-PRSMVPCNRE-----KVISFATISIDKSTYSRVLT 111
 119 FSGRMAASGMEVOTRPMFVQFPNATOTMNI RVLVLRPYDNLITLSQYVQVANSQW 178
 112 FOLSPMLSHLTHARLMLHV--PPSPFATLYLRIFGCGTTRCGSRFTLAHQTTSSGMH 169
 179 QLLALGPEAOAASQG--HTLELVP--ESQVAAHSLIL-----GWFSHRPVAAQVRYE- 228
 170 ALTPSSGRLSESSVTKQLQLEFRPLDNLSTARLPRLLDITAG--QQRPLELKTIRANE 227
 229 -GKHVRARRGIDCGGSRMCCROEFVDFREIGWMDWIIQPEGYAMNCTGOCPLHVAQM 287
 228 PCAGRRARRTPCESETPCLCCRRDHVDFQELGWRMDIQLQPEGYQOLNYSCGCPPLACS 287
 288 PGISAFHFAVNLKLANA--AAGTGRGSCCVPTSRRLSLLYYDRSDNIYKTDIPDMV 345
 288 PGISAFHFAVNSFLKANNPWPAGS---SCCVPTARRPLSLLYLDHNGVAKTDVDMV 343
 346 VEACGS 352
 344 VEACGS 350
 RESULT 6
 ID HBE_MOUSE STANDARD: PRT: 350 AA.
 AC 008717;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibin beta E chain precursor (Activin beta-E chain).
 GN INHBE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCB1_TxID-10090;
 RN 11)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver.
 RX MEDLINE-97096313; PubMed-8941337;
 RA Fang J., Yin W., Smiley E., Wang S.O., Bonadio J.;
 RT "Molecular cloning of the mouse activin beta E subunit gene."
 RL Biochem. Biophys. Res. Commun. 228:669-674(1996).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97224404; PubMed-9070865;
 RA Fang J., Wang S.O., Smiley E., Bonadio J.;
 RT "Genes coding for mouse activin beta C and beta E are closely linked
 and exhibit a liver-specific expression pattern in adult tissues."
 RL Biochem. Biophys. Res. Commun. 231:655-661(1997).
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
 CC FUNCTIONS SUCH AS HYPOTHALMIC AND PITUITARY HORMONE SECRETION,
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
 CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
 CC ACTIVINS.

CC -1- SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH
 CC ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.
 CC ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY
 CC SIMILARITY).
 CC -1- DEVELOPMENTAL STAGE: FIRST EXPRESSION IN EMBRYONIC LIVER IS
 CC DETECTED AT DAY E17.5.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC -----
 CC EMBL: U96386; AB53801.1; .
 CC HSSP: P12643; 3BMP.
 CC MGD: MGI:109269; Inhb.
 CC InterPro: IPR002400; GF_cysknot.
 CC InterPro: IPR001318; Inhibin_beta.
 CC InterPro: IPR001839; TGF-beta.
 CC Pfam: PF00019; TGF-beta.1.
 CC PRINTS: PR00438; GFCYSKNOT.
 CC PRINTS: PR00672; INHIBINBC.
 CC Prodom: PD000357; TGF-beta.1.
 CC SMART: SM00204; TGF-beta.1.
 CC PROSITE: PS00250; TGF-BETA_1; 1.
 CC Growth factor; Hormone; Glycoprotein; Signal.
 CC SIGNAL 1 21
 CC PROPEP 22 236
 CC FT CHAIN 237 350
 CC FT DISULFID 240 248 BY SIMILARITY.
 CC FT DISULFID 247 315 BY SIMILARITY.
 CC FT DISULFID 276 347 BY SIMILARITY.
 CC FT DISULFID 280 349 BY SIMILARITY.
 CC FT DISULFID 314 314 INTERCHAIN (BY SIMILARITY).
 CC CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 350 AA: 39057 MW: F37C76C8061D8A9D CRC64;
 Query Match 31.4%; Score 581.5; DB 1; Length 350;
 Best Local Similarity 37.7%; Pred. No. 1.4e-46;
 Matches 140; Conservative 66; Mismatches 110; Indels 55; Gaps 14;
 5 LLLALLFLPTTVVNPKEGCPACGAIFFDESQRELLDLAKSLDKLHLSQRPILS 64
 12 LLMALVWV-----QSTRSACPSGCGPTLAPQGERALVLELAKQILEGLHLSRPRT 64
 65 RYVSGALKTALQRLGRPR-----RETLLEHDQROEEYEIISFADTSSINQRLERH 116
 65 RPLPQALTRALRLQ-PRSMVPCNRE-----KVISFATISIDKSTYSRVLT 111
 117 FHSGRMAASGMEVOTRPMFVQFPNATOTMNI RVLVLRPYDNLITLSQYVQV 172
 112 FOLSPMLSHL-----YHARLMLHVPPSPGTYLH--IFRCGTRCGREFRFLAEH--QT 163
 173 NASGWYLLGPEAOAASQGHITEL-----VESQVAAHSLILGWF-SHRPVAQV 225
 164 TSSGHALTLTPSSGRLSESSVTKQLQLEFRPLDNLSTAGLPRLLDITAGQORPLELKI 223
 226 RYE--GKHVRARRGIDCGGSRMCCROEFVDFREIGWMDWIIQPEGYAMNCTGOCPLH 283
 224 RANEGAGARRARRTPCESETPCLCCRRDHVDFQELGWRMDIQLQPEGYQOLNYSCGCPH 283
 284 VAGMGISAFHFAVNLKLANA--AAGTGRGSCCVPTSRRLSLLYYDRSDNIYKTDI 341
 284 LAGSPGACASFAVNSFLKANNPWPAGS---SCCVPTARRPLSLLYLDHNGVAKTDV 339
 342 PMVVEACGS 352
 340 PMVVEACGS 350

RESULT 7
ID INHIB-CHICK STANDARD; PRT: 391 AA.
AC P27093: 073796: 391 AA.
DT 01-NOV-1995 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibin beta B chain precursor (Activin beta-B chain).
GN INHIB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Anseriformes; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Follicle;
RA Klingner H., Haleschek-Wiener J., Wohlrab B.K., Kuchler K., Wohlrab F.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=Ovary;
RA Hecht D.J., Davis A.J., Ryan I.M., Johnson P.A.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 311-381 FROM N.A.
RX MEDLINE=91029482; PubMed=2225063;
RA Mitrani E., Ziv T., Thomsen G., Shimon Y., Melton D.A., Brill A.;
RT In the hypothalamus of the chick.
RL Cell 63:95-501(1990).
CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC EMBRYONIC DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A HOMODIMER OF BETA-A.
CC ACTIVIN B IS A HOMODIMER OF BETA-B.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: Z71594: CAA96248.1: -
DR EMBL: AF055478: AAC14187.1: -
DR EMBL: M61166: AAA48568.1: -
DR EMBL: M57408: AAA03079.1: -
DR HSSP: P18075: 1BMP.
DR InterPro: IPR002400: GF_cysknoc.
DR InterPro: IPR001839: TGF-beta.
DR InterPro: IPR001111: TGF-beta.
DR Pfam: PF00019: TGF-beta: 1.
DR Pfam: PF00688: TGF-beta: 1.
DR PRINTS: PR00438: GRCYSKNOC.
DR PRODOM: PD000357: TGF-beta: 1.
DR SMART: SM00204: TGF-beta: 1.
DR PROSITE: PS00250: TGF-BETA: 1.
KM Growth factor; Hormone; Glycoprotein; Signal.
FT * SIGNAL. 1 25 POTENTIAL.

FT PROPEP 26 276 POTENTIAL.
FT CHAIN 277 391 INHIBIN BETA B CHAIN.
FT DISULFID 280 288 BY SIMILARITY.
FT DISULFID 287 356 BY SIMILARITY.
FT DISULFID 316 388 BY SIMILARITY.
FT DISULFID 320 390 BY SIMILARITY.
FT DISULFID 355 355 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 77 77 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 30 30 P -> PG (IN REF. 2).
SQ SEQUENCE 391 AA: 43608 MW: 060017BF33F7AF6C CRC64;
Query Match 30.1%; Score 556; DB 1; Length 391;
Best Local Similarity 33.4%; Pred. No. 3.7e-44;
Matches 129; Conservative 67; Mismatches 148; Indels 42; Gaps 10;
QY 1 MASSLLALLFLPTTVVNPRTGCPGACGAFDLESORELL----DLAKSILDKH 56
DB 14 LACGLLIGAAATPTP--PAGSSPDCTSCGFRPEPGKVGDFLAVRHLISRLQ 71
QY 57 LSORPLSRPVSGALKTALQRLGPRRETLLEHDQOE-----EYRI 99
DB 72 MRORPNTTHAVPKAAVATLAKHACK----VREDGRVELPSLDGASGAPRAHPVSI 127
QY 100 ISPADLSSINQRLPEFHFSGHMASGMEVQRTREFEVQ-PPH----NATQMINIRLV 154
DB 128 ISFAETDILASSRVLRYLFELISNEGONLFEVQASLWLYLKLPLYLEKSGRRKRVKYF 187
QY 155 LRYDNLITFSQYVOVNASGYOULLGPEAGACSGHLLTELVPESQVAHSSLL-- 212
DB 188 QDDPTNKNMNVKKVLDLRSGMHTFPMTEADIALFERGERRLNLDQEGCEYSVLP 247
QY 213 ---GWFSRPFVAAQVRV-EGKRVRRGIDOGSGRCCROEFVDEIGMNDWILQ 267
DB 248 YVDGESHHPFLVQARLADKNHRIKRGLEDGRTNLCCNQGFIDRLRLGMWILA 307
QY 268 PEYANMFTGQCPPLVAGMPGISAFHTAVYLKANA--AGTGRGSCVPTSRPLS 326
DB 308 PSQYGNVYCEGSPAVIAGPSSASFHTAVVQYRMRLNGTV--NSCIPITKLSTWS 365
QY 327 LLYYDRDSNIVKTDIPDMVVEACGS 352
DB 366 MLTFDEYIVKROVPMNIVECGCA 391
RESULT 8
ID INHIB-BOVIN STANDARD; PRT: 408 AA.
AC P42917:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibin beta B chain precursor (Activin beta-B chain).
GN INHIB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95112839; PubMed=7813465;
RA Thompson D.A., Cronin C.N., Martin F.;
RT Genomic cloning and sequence analyses of the bovine alpha-, beta A-
RT and beta B-inhibin/activin genes. Identification of transcription
RT factor AP-2-binding sites in the 5'-flanking regions by DNase I
RT footprinting.
RL Eur. J. Biochem. 226:751-764(1994).
CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION.


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DR InterPro: IPR001839, TGF-beta.
DR InterPro: IPR001111, TGF-beta.
DR Pfam: PF000019, TGF-beta. 1.
DR Pfam: PF000688, TGF-beta, propeptide. 1.
DR PRINTS: PR00438, GFCYSKNOR.
DR PRINTS: PR00671, INHIBINB.
DR ProDom: PD000357, TGF-beta. 1.
DR SMART: SM00204, TGF-beta. 1.
DR PROSITE: PS00250, TGF-beta.1.
DR Growth factor: Hormone: Glycoprotein: signal.
FT SIGNAL 1 28
FT PROPEP 29 292
FT CHAIN 293 407
FT DISULFID 296 304
FT DISULFID 303 372
FT DISULFID 332 404
FT DISULFID 336 406
FT DISULFID 371 371
FT CARBOHYD 93 93
FT CONFLICT 47 47
SQ SEQUENCE 407 AA: 45121 MW: 90316C83597B4B64 CRC64:

Query Match 29.6% Score 548.5; DB 1; Length 407;
Best Local Similarity 33.3%; Pred. No. 1.9e-43;
Matches 134; Conservative 66; Mismatches 145; Indels 57; Gaps 13;

QY 2 ASSLLALLFL-----TPTTVVNPRTGCP-----CPACGAIFFLESOREL 42
D 12 ACILLLAGNIGPEAMGSPRPFPAPAPPPPPGSGSODITCTSCG---FRREEL 67
QY 43 -----LIDAKKSLILKHLKSLSPPIISRYSGALKTALQRLR-GPRR-----TLEH-- 90
D 68 GRVDGDFLEAVKRIHLRLQMRGNPTTHAVPKAAWYALRLKLAGVRDGRVETPHLD 127
QY 91 -----DQROEEYEISFADTDLSSINQTRLEFHFSGRMASGMEVQTRFMFVQ-FPH 142
D 128 GHASPGADGQERSEIISFAETDGLASSRRLKLPFTISNEGONLFFVQASLMLTKLPPY 187
QY 143 -----NATQTNIRVLVLRPYDTNLTLTSQVYVQVNASGWYQLLGPBAQCSOGLTLE 198
D 188 VLEKSGSRKRVKVVYFQEGCHGRMNMNVEKRVLDKRGSMHTFPLEIAQLAFERGERLN 247
QY 199 LVPESQVAHSSLLIGWF-----SHRFVAQVAV-BGKRRVRRRGIDCGGSRMCCRQ 251
D 248 LDVQCCSQCELAIVPVVDGEEHRRFVAVQARLGSRRIKRGECGGRNLCCRQ 307
QY 252 FFVDFREIGNMDWITQEGYAMNCTGOCPLHYAGMGICASFHTAVLNLKKNAA-AGT 310
D 308 FFIDFRILGNMDWITQEGYAMNCTGOCPLHYAGMGICASFHTAVLNLKKNAA-AGT 310
QY 311 TGRGCCVPPSRPRLSLLYDRDSNIVKTDIPMVEACGCS 352
D 368 V--NSCICPTKLTSMMLYFDDEYNIVKRDVPMNIVECCGA 407

RESULT 10
ID INHB_PIG STANDARD: PRT: 349 AA.
AC PD0088;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Inhibin beta B chain precursor (Activin beta-B chain) (Fragment).
GN INHB.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE-Ovarian follicular fluid;
RC MEDLINE=86092207; PubMed=2417121;
RA "Masson A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,

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RA Guillemin R., Niall H., Seeburg P.H.;
RT "Complementary DNA sequences of ovarian follicular fluid inhibin show
RT precursor structure and homology with transforming growth
RT factor-beta";
RL Nature 318:659-663(1985).
RN 12
RP SEQUENCE OF 235-249.
RX MEDLINE=92355604; PubMed=1644823;
RA Nakamura T., Asashima M., Ito Y., Takio K., Uchiyama H., Moriya N.,
RA Arizumi T., Yashiro T., Sugino K., Titani K., Sugino H.;
RT "Isolation and characterization of native activin B";
RL J. Biol. Chem. 267:16385-16389(1992).
CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
CC RESEPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A HOMODIMER OF BETA-A.
CC ACTIVIN B IS A HOMODIMER OF BETA-B.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
CC EMBL: X03267; CAA27021.1;
CC DR PIR: A01394; WPCGB.
CC DR HSP: P18075; IBM.
CC DR InterPro: IPR001839, TGF-beta.
CC InterPro: IPR001111, TGF-beta.
CC Pfam: PF000019, TGF-beta. 1.
CC Pfam: PF000688, TGF-beta, propeptide. 1.
CC ProDom: PD000357, TGF-beta. 1.
CC SMART: SM00204, TGF-beta. 1.
CC PROSITE: PS00250, TGF-beta.1.
CC Growth factor: Hormone: Glycoprotein.
CC NON_TER 1 234
CC PROPEP <1 234
CC CHAIN 235 349
CC DISULFID 238 246
CC DISULFID 245 314
CC DISULFID 274 346
CC DISULFID 278 348
CC DISULFID 313 313
CC CARBOHYD 35 35
SQ SEQUENCE 349 AA: 39354 MW: C571E91ADAD5E7 CRC64:

Query Match 29.5% Score 546; DB 1; Length 349;
Best Local Similarity 35.8%; Pred. No. 2.7e-43;
Matches 120; Conservative 65; Mismatches 122; Indels 28; Gaps 9;

QY 44 IDLAKKSILDKLQSLRPLSRVSGALKTALQRLR-GPRR-----TLEH----- 90
D 17 LEAVKRIHLNKLQMRGNPTTHAVPKAAWYALRLKLAGVRDGRVETPHLDGHASFGA 76
QY 91 DQROEEYEISFADTDLSSINQTRLEFHFSGRMASGMEVQTRFMFVQ-FPH-----NAT 145
D 77 DQERSEIISFAETDGLASSRRLKLPFTISNEGONLFFVQASLMLTKLPPYLEKSR 136
QY 146 QTMNIRVLVLRPYDTNLTLTSQVYVQVNASGWYQLLGPBAQCSOGLTLELVPEQV 205

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Db 137 RKVRKVFQEGHGRDMDVYKRDVLRSGMHTLPLEATQALFERGERRLNDVQCG 196
 Oy 206 ANSLILCMF-----SHRPVAAQVR-ECKHVRRRGIDCGSRMCCROEFVFPRE 258
 Db 197 CQELAVVFPVPCGESHRRFPVYQARLGDNRHRRKRGLECDRTNLCRQOFPIDFRL 256
 Oy 259 IGMNMTIOPEYANNFCGCGPLVAGMPGISAFHVAHLNLKANA-AGTGRGSCC 317
 Db 257 ICMSDMTIAPTGYGNYCGSCPAFLAGPSPASSFHTAVVNOTRMKGLNPTV--NSCC 314
 Oy 318 VPTSRPLSLYYDRSDNIVKTDIPDMVVEACGCS 352
 Db 315 IPRKLTSMMLTFDEEYNVKKRDVPMVVEEGCA 349

RESULT 11
 ID IHA_PIG STANDARD: PRT: 424 AA.
 AC P03970:
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibin beta A chain precursor (Activin beta-A chain).
 GN INHBA.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Follicular fluid;
 RX MEDLINE=86092207; PubMed=2417121;
 RA Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,
 RA Guillemin R., Nall H., Seeburg P.H.;
 RA Complementary DNA sequences of ovarian follicular fluid inhibin show
 RT precursor structure and homology with transforming growth
 RT factor-beta.";
 RL Nature 318:659-663(1985).
 RN [2]
 RP SEQUENCE OF 309-323.
 RC TISSUE-Follicular fluid;
 RX MEDLINE=92355604; PubMed=1644823;
 RA Nakamura T., Aashima M., Eto Y., Takio K., Uchiyama H., Moriya N.,
 RA Arikawa T., Yashiro T., Sugino K., Titani K., Sugino H.;
 RA "Isolation and characterization of native activin B.";
 RL J. Biol. Chem. 267:16385-16389(1992).
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
 CC FUNCTIONS SUCH AS HYPOTHALMIC AND PITUITARY HORMONE SECRETION,
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
 CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
 CC ACTIVINS.
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X03266; CAA27020.1; -;
 DR PIR: A01393; WPGBA.

DR HSSP: P18075; 1BMP.
 DR InterPro: IPR002400; GF_cysknob.
 DR InterPro: IPR000491; Inhibin_beta.
 DR InterPro: IPR01839; TGF-beta.
 DR InterPro: IPR01111; TGF-beta.
 DR Pfam: PF00019; TGF-beta.1.
 DR Pfam: PF00688; TGF-beta-propeptide.1.
 DR PRINTS: PR00438; GFCSKNOT.
 DR PRINTS: PR00670; INHIBINBA.
 DR PRODOM: PD000357; TGF-beta.1.
 DR SMART: SM00204; TGF-beta.1.
 DR PROSITE: PS00250; TGF-BETA_1; 1.
 DR Growth factor: Hormone; Glycoprotein; signal.
 KW SIGNAL
 FT SIGNAL 1 20
 FT PROPEP 21 308
 FT CHAIN 309 424 INHIBIN BETA A CHAIN.
 FT DISULFID 312 320 BY SIMILARITY.
 FT DISULFID 319 389 BY SIMILARITY.
 FT DISULFID 348 421 BY SIMILARITY.
 FT DISULFID 352 423 BY SIMILARITY.
 FT DISULFID 388 388 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 165 165 N-LINKED (GLCNAG...)(POTENTIAL).
 SQ SEQUENCE 424 AA; 47476 MW; 436BC2226FPAF52 CRC64;

Query Match 29.4%; Score 543; DB 1; Length 424;
 Best local Similarity 31.6%; Pred. No. 6,6e-43;
 Matches 133; Conservative 67; Mismatches 141; Indels 80; Gaps 11;

Oy 6 LALLFLPTTYVNPKEG-----PCPACWGAIF--DLESORELLDLAKSILDKLHS 58
 Db 10 LASCWIVNNSPTPGSGHSAAPDCPSALTLPKDVPNSQPEKVEAVKKHILMLHLK 69
 Oy 59 QRPILSRPVSFGALKTALRLR-----GPRRETLLEHDOQEYEIISF 102
 Db 70 KRDPYQVPYKALLNALIKRLHVGKGVGYELDDIGRARE--NELMEQSEITTF 126
 Oy 103 ADPLDLSINQTRLEFHFSGMASGMEVQTRFMFVQEPH-NATQF-MNIRYL----- 153
 Db 127 AEAGTA---RKTLPFEISKGSIDLVERAEIWLFLKVPKANRTKVSIRLFOOORAPQ 183
 Oy 154 -----VLRPDYTNLITLSQYVQVNSGWOLLGFEQAACSGHLTLELPE 202
 Db 184 GSADAGEADVDVPEPEKSEVLISEKVDARKSTWHIFPVSSIRPLDDQGSALDIRTA 243
 Oy 203 SOVAH-----SSLIIG-----WFSRRPFAAQR--VEGKH 231
 Db 244 CEQCHETGASLVLLGKKKKKEEABGRKRDGAGVDEKEDSHRPLMLQAROSEHPR 303
 Oy 232 RVRRRGIDCGGSRMCCROEFVDFREIGMDWITIOPEYAMNFCGCGPLVAGMPGIS 291
 Db 304 RRRRGLECGKVNICCKQFVPSFDIGMDWIIIPSGYHANYEGEGCPSHIAGTSSS 363
 Oy 292 ASFTAVLNLKANAAGTGRGSCCVTSRRPLSLYYDRSDNIVKTDIPDMVVEACGC 351
 Db 364 LSFHSTVINYHMRGHSFRANLKSVCPTKLKPMNMLYDDQONIIKDIQMYVEEGCC 423

Oy 352 S 352
 Db 424 S 424

RESULT 12
 ID IHA_HUMAN STANDARD: PRT: 426 AA.
 AC P08476; 014599;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Inhibin beta A chain precursor (Activin beta-A chain) (Erythroid
 DE differentiation protein) (EDF).
 GN INHBA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
 ON NCBI_TaxID=9606;
 [1]
 RX SEQUENCE FROM N.A.
 RX MEDLINE=86186863; PubMed=3754442;
 RA Mason A.J., Niall H.D., Seeburg P.H.;
 RT "Structure of two human ovarian inhibins.";
 RL Biochem. Biophys. Res. Commun. 135:957-964(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88190086; PubMed=3267209;
 RA Murata M., Eto Y., Shibai H., Sakai M., Muramatsu M.;
 RT "Erythroid differentiation factor is encoded by the same mRNA as that
 of the inhibin beta A chain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:2434-2438(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92135888; PubMed=1777673;
 RA Tanimoto K., Hada S.I., Ueno N., Murakami K., Fukumizu A.;
 RT "Structure and sequence analysis of the human activin beta A subunit
 gene.";
 RL DNA Seq. 2:103-110(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Glessip D., Dubucque T., Graves T., Duckles G.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 311-426 FROM N.A.
 RX MEDLINE=87005283; PubMed=3758355;
 RA Stewart A.G., Milborrow H.M., Ring J.M., Crowther C.E., Forage R.G.;
 RT "Human inhibin genes. Genomic characterisation and sequencing.";
 RL FEBS Lett. 206:329-334(1986).
 RN [6]
 RP SEQUENCE OF 311-426 FROM N.A.
 RC TISSUE=Testis;
 RA Berg H., Walter M., Northmann W.;
 RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
 RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
 INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
 FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
 GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
 ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
 EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
 SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
 ACTIVINS.
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
 INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL: M13436; AAA59168.1;
 DR EMBL: X04447; CAA28041.1;
 DR EMBL: X57578; CAA40805.1;
 DR EMBL: X57579; CAA40805.1; JOINED.
 DR EMBL: X57579; CAA40805.1;
 DR EMBL: AC005027; AAD43185.1;
 DR EMBL: J03634; AAA35787.1;
 DR EMBL: A14423; CAA01159.1;
 DR EMBL: X72498; CAA51163.1;
 DR EMBL: A30884; A30884.
 DR EMBL: A30884; A30884.
 DR PTR: B24248; B24248.

DR PIR: B23556; B23556.
 DR PIR: S30488; S30488.
 DR HSP: P18075; IIMP.
 DR MIM: 147290;
 DR InterPro: IPR002400; GF_cysknot.
 DR InterPro: IPR000491; Inhibin_beta.
 DR InterPro: IPR001839; TGF-beta.
 DR InterPro: IPR001111; TGF-beta.
 DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGF-beta; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR PRINTS: PR00670; INHIBINB.
 DR ProDom: PD000357; TGF-beta; 1.
 DR SMART: SM00204; TGF-beta; 1.
 DR SMART: PS00250; TGF-beta; 1.
 DR Growth factor; Hormone; Glycoprotein; Signal.
 KW SIGNAL
 FT PROPEP 21 310
 FT CHAIN 311 426
 FT DISULFID 314 322
 FT DISULFID 321 391
 FT DISULFID 350 423
 FT DISULFID 354 425
 FT DISULFID 390 390
 FT CARBOHYD 165 165
 FT CONFLICT 377 379
 SO SEQUENCE 426 AA; 47442 MW; 201CDEDF90CB6919 CRC64;
 RMR -> AC (IN REF. 6).
 N-LINKED (GLCNAC...) (POTENTIAL).
 INTERCHAIN (BY SIMILARITY).
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 INHIBIN BETA A CHAIN.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 POTENTIAL.

Query Match 29.28; Score 540; DB 1; Length 426;
 Best Local Similarity 31.24; Pred. No. 1,3e-42;
 Matches 132; Conservative 70; Mismatches 139; Indels 82; Gaps 11;

QY 6 LALLFLPTPTVNVNPKTEG-----PCPACGALF--DLESQRELLDLAKKSLDKLHLS 58
 DB 10 LIASWIVVNSPPGSGHSADPCSCALALPDPVNSQPEVNEAVKHTLNLHLK 69
 QY 59 QRPILSRPVSRLGKLTALQRLR-----GPRRETLLEHDOREVEIISF 102
 DB 70 KRDPVQGVPAALALMLIRKLHGKVGENGVEIEDDIGRAM--NELMOTSILTF 126
 QY 103 ADTDLSTINQRLFLHNSGMAEMEKROTREPVQFPH-NATOT-ANIRVLYLRP-- 158
 DB 127 AE---SGTARTLHFEISKSGSDLSVERAEVWLFVKVRANTRTKRYIRLFQOKHPQ 183
 QY 159 -----DTNLTFSQVYVNASGWYQLLGPBAQACSGHLLTEL--- 199
 DB 184 GSDTGERAEVGLKGRSELLESEKYDARKSTWVFFVSSIQRLDQKSSLDVRIA 243
 QY 200 VPESQVAHSSLT-----GWFSRHPVAQVR--VEG 229
 DB 244 CECCQEGASIVLLGKKKKKEEGEGKKKGCGAGADEKEKGRPLMLQAROSDH 303
 QY 230 KHRVRRRGIDCCGGRNCCQGEFFVDFRELGNWDWLTIOEGYAMNFCGQCLHVAQMP 289
 DB 304 PHRRRRGLECDGVNVCCKKFFVSKDIGNWDWLIASGVHANYCEDECPSHIATSG 363
 QY 290 ISAFHTAVNLKANAAGTGRGSCCVPTSRPLSLIYVRODSINYKTOIPDMVNEAC 349
 DB 364 SLSLFSHTVYHNRMGHSPFALAKSCVPTRLRPSMLIYDQGNITIKDIQNNIVEEC 423
 QY 350 GCS 352
 DB 424 GCS 426
 RESULT 13
 ID INHIBIN_MOUSE STANDARD: PRT: 424 AA.
 AC Q04998;
 DT 01-FEB-1994 (rel. 28, Created)
 DT 01-FEB-1994 (rel. 28, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Inhibin beta A chain precursor (Activin beta-A chain).

```

OS INHBA.
NS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE:93321614; PubMed:8330535;
RA Albano P.M., Groome N., Smith J.C.;
RT "Activins are expressed in preimplantation mouse embryos and in ES
RT and EC cells and are regulated on their differentiation.";
RL development 117:711-723(1993).
CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A HOMODIMER OF BETA-A.
CC ACTIVIN B IS A HOMODIMER OF BETA-B.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -1- TISSUE SPECIFICITY: UTERUS, OVARY, AND LIVER.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: X69619; GMA49325.1; -.
DR PIR: S31440; S31440.
DR HSP: P18073; IBMP.
DR MGD: MG1:96570; IBhda.
DR InterPro: IPR002400; GF_cysknoc.
DR InterPro: IPR000491; Inhibin_betaA.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta.1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR PRINTS: PR00438; GF_CYSKNOT.
DR PRINTS: PR00670; INHIBINBA.
DR Prodom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
KW Growth factor; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 20
FT PROPEP 1 308
FT CHAIN 309 424 INHIBIN BETA A CHAIN.
FT DISULFD 312 320 BY SIMILARITY.
FT DISULFD 319 389 BY SIMILARITY.
FT DISULFD 348 421 BY SIMILARITY.
FT DISULFD 352 423 BY SIMILARITY.
FT DISULFD 388 388 INTERCHAIN (BY SIMILARITY).
FT CARBOHD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 424 AA; 47392 MW; 80C251B8754A7213 CRC64;

Query Match 29.1%; Score 538; DB 1; Length 424;
Best Local Similarity 32.1%; Pred. No. 1,9c-42;
Matches 136; Conservative 68; Mismatches 134; Indels 86; Gaps 14;

6 LALLFLFTTIVNPKTE-----PCPACGMAIFDL-----ESQRELLDLAKKSLDKL 55
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
10 LASCMTIVRSPTPSSBCHGAPDPCSC--ALATLPKCGPNSQEP--WEAVAKKHLINML 66

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OY      HLSORPLISRPVSGALKTALQRLR-----GPRRTLEHDDOROEEYL 99
Db      67 HLKKRPDVTQVPVKALLNMRKLHVKGVBENGVEYLEEDIGRAEK---NELMDQTSEI 123
OY      100 ISFADTLLSINOTRLEFHFSGRNASGMERYQRTEMFFVOYPH-NATQTMIRVLVLRP 157
Db      124 ITPAE--SGTARKTLHPHEISKEGSDLSVERAEVWFLFKVPKANRRTRKVTITRPOOK 180
OY      158 Y-----DTNLVTYSQYVVQVVASGWYOLLGPREQAACSGGHILTEL 199
Db      181 HPQGSLDTGDEAEEKGLKERSELLTEKVVDARKSTWHMIFPVSSSIQRLDDCKSSLDV 240
OY      200 ---VESVAHSSLTL-----GMF-----SHRPVAQVR--VE 228
Db      241 RIACEOCESASLVLYLGKKKKKEVDDGDKKKDDSGGLEBEKQSHRPFMLIMDAQSED 3000
OY      229 GKHRVRRRGIDCOGSRMCQRQEFVDFREIGNDWMIIQEGYAMNFCTGOCPLHAVAGMP 288
Db      301 HPHRRRRRGLEDGDGVNITCCKKQFPVSFKDIGMWDMIAPSGYHANCCEBECPSHIAGTS 360
OY      289 GTSASFHTAVLNLKANAAGCTGRCGCVCVPTSRRLPSLLTYFDNSNIYVTDIPDMVYA 348
Db      361 GSLSLFHSHTVINHYRMRGSPFANLKSVCVPTKLRPMSLMYYDDGGNIKKKDIONMIVEE 420
OY      349 CGCS 352
Db      421 CGCS 424

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RESULT 14

ID	IHB#
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DT 01-1

1b-C

GN
JNHT

March

BN [1]

RX	MED
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RT "Rat

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CC beta

CC use

cc ent

[illegible]

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CC EMBL: M37482; AAA4136.1;
DR PIR: B40056; B40056.
DR HSSP: P18075; 1BMP.
DR InterPro: IPR002400; GF_cyskn0t.
DR InterPro: IPR000491; Inhibin_betaa.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGFb.N.
DR Pfam: PF000019; TGF-beta.1.
DR Pfam: PF00688; TGFb_propeptide.1.
DR PRINTS: PR00438; GFCYSKN0T.
DR PRINTS: PR00670; INHIBINB.
DR ProDom: PD000357; TGF-beta.1.
DR SMART: SM00204; TGFb.1.
DR PROSITE: PS00250; TGF_BETA.1.1.
KW Growth factor; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 20
FT PROPEP 21 308
FT CHAIN 309 424
FT DISULFID 312 320
FT DISULFID 319 389
FT DISULFID 348 421
FT DISULFID 352 423
FT DISULFID 388 388
FT CARBOHYD 165 165
SQ SEQUENCE 424 AA: 47406 MW: 82DAF7917FA50984 CRC64;

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Query Match 29.1%; Score 538; DB 1; Length 424;
Best Local Similarity 32.1%; Pred. No. 1.9e-42;
Matches 136; Conservative 68; Mismatches 134; Indels 86; Gaps 14;

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OY 6 LLALEFLPTTVVNPRTG-----PCPACMGAIIFDL-----ESORELLDLAKKSIIDKL 55
DB 10 LLASCMIIIVRSPPRGSGHGAAPDCPC--ALATLPKDGNSQPE--NVEAVKKHIIIML 66
OY 56 HLSORPILSRPVSKALTAOLRL-----GPRRETLLEHDQROEEYEI 99
DB 67 HLKRPDVTQVPKAKALLNAIRKLHVGKGVGEVIEDDIGRAEM--NELMEQTSSEI 123
OY 100 ISFADTDLSSINOTLEFHFSGRMASGMEVROTFRMPFPH--NAQOT--NINIVLVLRP 157
DB 124 ITFAE--SGTARKTLHEIKESGDSLVRAEAWLFLKVPKAKNRRTKTVLIPDOOK 180
OY 158 Y-----DTNLTLTQYVQVNAAGVYQLLPEAQAACSGHLEL 199
DB 181 HPGSLDMDGAEEKGLKGERSELLSEKVVDAKSTWHIPVSSIQRLLDGKSSLDV 240
OY 200 ---VPSQVAHSSLL-----GPF-----SHRPVAAQVR--VE 228.
DB 241 RIACEQCCESGASVLLGKKKKKKKVDGKKKSDGDLGEEKDSHRPFLMLDAROSD 300
OY 229 GKHYRRRGIDCCGSRMCQROEFFVDREITGMNDWIIIOPEGYAMNCTGCCPLHVGMP 288
DB 301 HPHRRRRRGLEGCDKQVNCCKKQFFVSKDIGNMDWIIIPSGYANVCCEGCPSHIAGTS 360
OY 289 GISSPHTAVLNLKANAAGCTGSGCCVPTSRRLSLVYDRDSINVKTDIPMVEEA 348
DB 361 GSSLSFHSSTVINHYRMHGHSPFANLKSCCVPTKLRPMSTMYYDDGQNIKKIDQNMIVEE 420
OY 349 CGCS 352
DB 421 CGCS 424

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RESULT 15
INHA_HORSE STANDARD; PRT; 426 AA.
AC PSS102;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibin beta A chain precursor (Activin beta-A chain).
GN INHA...

```

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OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary.
RX MEDLINE=96031670; Pubmed=7548399;
RA Yoshida S., Yamamouchi K., Hasegawa T., Ikeda A., Suzuki M.,
RA Chang K., Matsuyama S., Nishihara M., Takahashi M.;
RT *Molecular cloning of cDNA for equine ovarian inhibin/activin beta A
RT subunit.*;
J. Vet. Med. Sci. 57:469-473(1995)
CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC EMBRYONIC DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A HOMODIMER OF BETA-A.
CC ACTIVIN B IS A HOMODIMER OF BETA-B.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
DR EMBL: D50326; BAO8862.1;
DR HSSP: P18075; 1BMP.
DR InterPro: IPR002400; GF_cyskn0t.
DR InterPro: IPR000491; Inhibin_betaa.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGFb.N.
DR Pfam: PF000019; TGF-beta.1.
DR Pfam: PF00688; TGFb_propeptide.1.
DR PRINTS: PR00438; GFCYSKN0T.
DR PRINTS: PR00670; INHIBINB.
DR ProDom: PD000357; TGF-beta.1.
DR SMART: SM00204; TGFb.1.
DR PROSITE: PS00250; TGF_BETA.1.1.
KW Growth factor; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 20
FT PROPEP 21 310
FT CHAIN 311 426
FT DISULFID 314 322
FT DISULFID 321 391
FT DISULFID 350 423
FT DISULFID 354 425
FT DISULFID 390 390
FT CARBOHYD 165 165
SQ SEQUENCE 426 AA: 47709 MW: E481060B8368A77D CRC64;

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Query Match 28.9%; Score 534; DB 1; Length 426;
Best Local Similarity 31.2%; Pred. No. 4.6e-42;
Matches 132; Conservative 68; Mismatches 141; Indels 82; Gaps 11;

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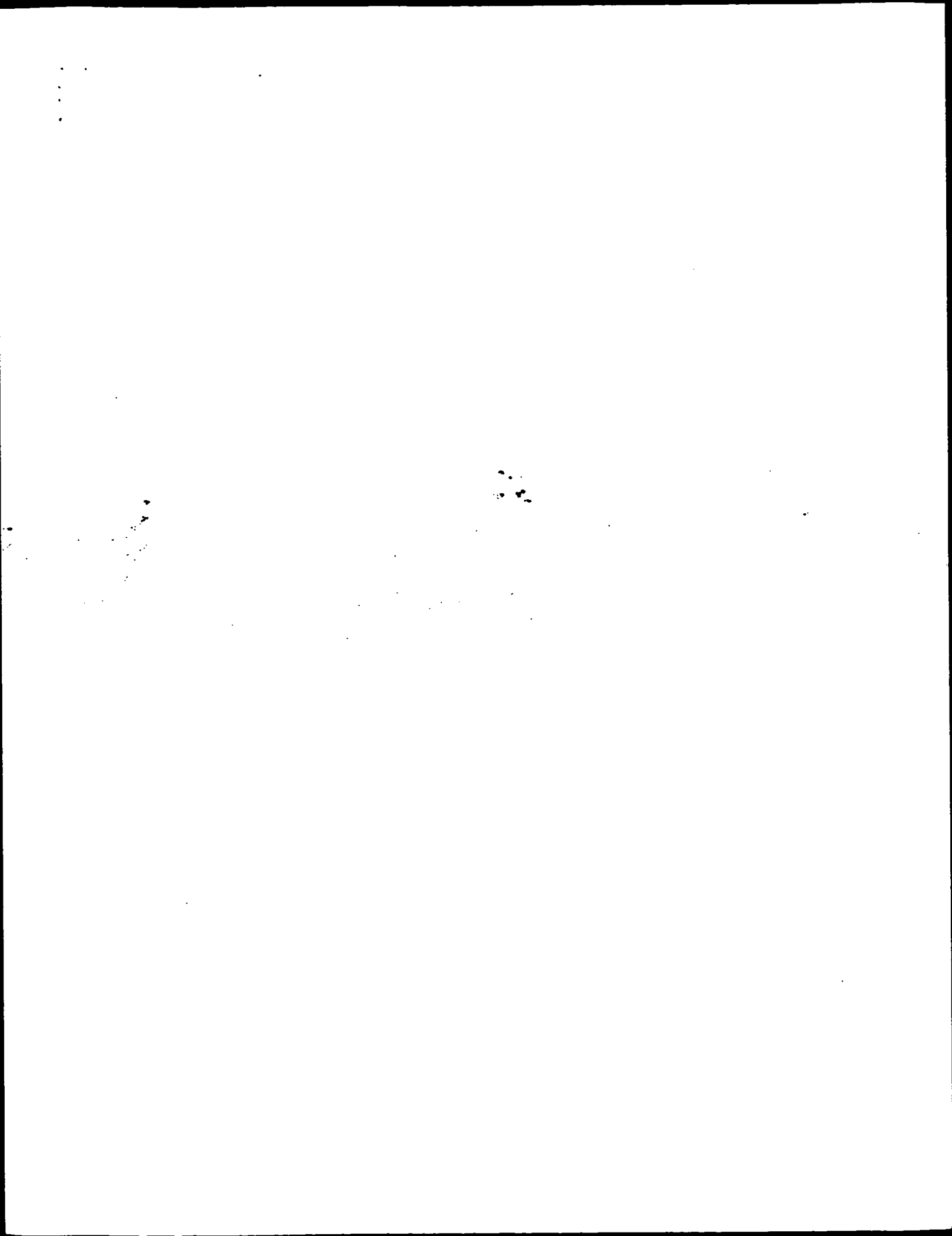
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OY 6 LLALEFLPTTVVNPRTG-----PCPACMGAIIFDL-----ESORELLDLAKKSIIDKLHS 58
DB 10 LLASCMIIIVRSPPRGSGHGAAPDCPC--ALATLPKDGNSQPE--NVEAVKKHIIIMLHK 69
OY 59 QRPILSRPVSKALTAOLRL-----GPRRETLLEHDQROEEYEIISF 102

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Db 70 KRPDTQPVPKAALLNATIRKLHVGVGNGVEIEDDIGRAEM---NELMEQTSITTF 126
QY 103 ADTDLSSINOTRLEFHFSGRMASGMEVROTRMFPVOPH-NATOT-MNIRVLVLRPY-- 158
Db 127 AE---SCTARKTLHFEISKEGSDLSVERAEVWLFKVPKANRTRSKYTIRLLOQKHQ 183
QY 159 -----DTNLTLTSGYVYQVNASGWYOLLGPBAQACSCGHITLTYPE 202
Db 184 GSDTREAEAEADLMEERSEQLISEKVVDARKSTWHIFPVSSIORLDOCKSSLDIRIA 243
QY 203 SOVAH---SSLILG-----WFSRPFVAOVR--VEG 229
Db 244 CDQCHETGASLVLLGKKKKKEEGEGKKKDGEGAGAGVDEKEQSHRPFLLMLQARQSEDH 303
QY 230 KHRVRRGIDCQGGSRMCCROEPFVDFREIGWMDWIIQPEGYAMNFTGQCPHVGMPG 289
Db 304 PHRRRRGLECDGKVNICKKQFVSEFKIDGMDWIIAPSGYHANYCEGECPSHIAGTSG 363
QY 290 ISAPHTAVLNLKANAAGTTGRGSCCVPTSRRLSLIYYDRDSNIVKTDIPDMVVEAC 349
Db 364 SSLSHSTVINOYRLRGHNPPANLKSQCVPTKLRPMMLYYDDGQNIKKDIONMIVEEC 423
QY 350 GCS 352
Db 424 GCS 426

Search completed: October 12, 2002, 02:06:56
Job time : 15.5 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 23:57:49 ; Search time 42 Seconds

(without alignments)
1449.862 Million cell updates/sec

Title: us-09-684-383-4

Perfect score: 1850
Sequence: 1 MASSLLALLFLPTTVNP.....DSNYKTDIPMWVACGCS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *
15: SP viirus: *
16: SP bacteriophage: *
17: SP archaea: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	699.5	37.8	367	13	Q91696 xenopus lae
2	587.5	31.8	350	11	Q91XN3 Q91XN3 mus musculu
3	566.5	30.6	370	13	Q91350 xenopus lae
4	545.5	29.5	395	15	Q9PWC6 Q9PWC6 anguilla ja
5	537	29.0	426	4	Q9HBP0 Q9HBP0 homo sapien
6	533.5	28.8	393	13	Q90261 brachydantio
7	528	28.5	413	13	Q98860 cynops pyr
8	527	27.0	392	13	Q9PWR8 Q9PWR8 carassius a
9	499	26.4	424	13	Q98SP9 Q98SP9 melagris g
10	488.5	26.0	404	13	Q9PWC5 Q9PWC5 carassius g
11	368	19.9	119	6	Q9SKP1 Q9SKP1 allurus fu
12	367.5	19.9	119	13	Q42125 pagrus majo
13	367	19.8	119	6	Q95N79 Q95N79 alluropoda
14	367	19.3	119	6	Q95KP2 Q95KP2 ursus malay
15	357	19.3	138	13	Q9W6T9 Q9W6T9 brachydantio
16	356	19.2	115	13	Q9DGF1 Q9DGF1 cyprinus ca

17	356	19.2	115	13	Q9DGE9 Q9DGE9 cyprinus ca
18	356	19.2	115	13	Q9DGE6 Q9DGE6 oryzias lat
19	350	18.9	115	13	Q9DGF0 Q9DGF0 cyprinus ca
20	341	18.4	115	13	Q9DGE7 Q9DGE7 oryzias lat
21	334	18.1	115	13	Q9DGE2 Q9DGE2 cyprinus ca
22	331.5	17.9	115	13	Q9DWC9 Q9DWC9 morone saxa
23	331.5	17.9	115	13	Q9DWC8 Q9DWC8 morone amer
24	331	17.9	115	13	Q9DGE8 Q9DGE8 oryzias lat
25	330.5	17.6	115	13	Q9DWC6 Q9DWC6 umbrina cir
26	325	17.6	115	13	Q9DWC7 Q9DWC7 salmo salar
27	324.5	17.5	115	13	Q9DWC1 Q9DWC1 oncorhynch
28	322.5	17.4	115	13	Q9DWC2 Q9DWC2 oncorhynch
29	322	17.4	115	13	Q9DWC3 Q9DWC3 cynops pyr
30	321	17.4	120	13	Q9DWC4 Q9DWC4 oncorhynch
31	318	17.2	115	13	Q9DWC5 Q9DWC5 brachydantio
32	317	17.1	115	13	Q9DWC6 Q9DWC6 salmo salar
33	314.5	17.0	115	13	Q9DWC7 Q9DWC7 morone chry
34	313.5	16.9	115	13	Q9DWC8 Q9DWC8 oreochromis
35	310	16.8	115	13	Q9DWC9 Q9DWC9 sparus aur
36	309.5	16.7	115	13	Q9DWC10 Q9DWC10 salvelinus
37	306.5	16.6	115	13	Q9DWC11 Q9DWC11 carassius a
38	300.5	16.2	115	13	Q9DWC12 Q9DWC12 carassius b
39	295.5	16.0	115	13	Q9DWC13 Q9DWC13 ictalurus p
40	288	15.6	115	6	Q9DWC14 Q9DWC14 equus cabal
41	287	15.5	115	6	Q9DWC15 Q9DWC15 drosophila
42	286	15.5	115	6	Q9DWC16 Q9DWC16 macaca fasc
43	285	15.4	115	6	Q9DWC17 Q9DWC17 carassius a
44	283.5	15.3	115	6	Q9DWC18 Q9DWC18 drosophila
45	283	15.3	115	6	Q9DWC19 Q9DWC19 bos taurus

ALIGNMENTS

RESULT 1

ID	Q91696	PRELIMINARY:	PRT:	367 AA.
AC	Q91696:			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	ACTIVIN D PRECURSOR.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RX	MEDLINE=95275314; PubMed=7755637;			
RA	Oda S., Nishimatsu S., Murakami K., Ueno N.;			
RT	*Molecular Cloning and functional analysis of a new activin beta			
RT	subunit: a dorsal mesoderm-inducing activity in Xenopus.*;			
RL	Biochem. Biophys. Res. Commun. 210:581-588(1995).			
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			
DR	EMBL: D49543; BAA08494.1; -			
DR	HSSP: P12643; 3BMP.			
DR	InterPro: IPR002400; GF_cysknot.			
DR	InterPro: IPR001839; TGF-beta.			
DR	InterPro: IPR001111; TGF-beta.			
DR	Pfam: PF00019; TGF-beta. 1.			
DR	Pfam: PF00688; TGF-beta. 1.			
DR	PRINTS: PR00438; GFCYSKNOT.			
DR	ProDom: PD000357; TGF-beta. 1.			
DR	SMART: SM00204; TGF-beta. 1.			
DR	PROSITE: PS00250; TGF-beta. 1.			
DR	GlycoProtein: Signal.			
FT	SIGNAL			
FT	CHAIN			
FT	SEQUENCE			
SO	SEQUENCE			
Query Match	367 AA;			
	41729 MW;			
	C7E6334BD606FA04 CRC64;			
	37.8%; Score 699.5; DB 13; Length 367;			

Best Local Similarity 39.38; Pred. No. 1,1e-61;
Matches 145; Conservative 65; Mismatches 122; Indels 37; Gaps 7;

QY 6 L1ALFLPTTTPVVPKTEGPCPACWCAIFDLESORELLDLAKSLDKLHLSORPLIS 65
DB 14 L1TLGLAALASTGGLTKKSCPCSG-----YQKVEYMIELAKQOILQKHLKERPI 67
QY 66 PVSFGALKTALOR--LKGPRRETL-----EHQOEYEITISFADTDLSSINOT 113
DB 68 PVPKGAVALNLRHLKPRMEGLFGSWSNDSENTEDTQOQSEYIISFAETETYNENSI 127
QY 114 RLEFHSGRMAAGMEVOTRPFVOPPHNATOTMINIRVLRYPDNLTLTSQYVQVN 173
DB 128 TLNFGFTRDKESAHVLAAILMLFPAKNTSQONETIRLVQDAYSRRLLISKLEPR 187
QY 174 ASGWYOLLGHEAQAACSGHLEL-----VPSQVAHSSLLLGWFSHPPVAAQ 224
DB 188 WTGQOTSLKSMLOTFPDGKNSIQLELNCDCQDVPLANPN-----SHOPFLVAAQ 240
QY 225 VRV-EGKHVRARRGIDCGGRMCCROEFVDFREIGMNMIIOPEGYQINVCMLCPMH 283
DB 241 AKVHOSHATKRSKLNCDQNSNLCCKRDYVDFDGMWMTIKPEGYQINVCMLCPMH 300
QY 284 VAGHGISASFTAVLNLKANAAGTTGSGCCVPTSRPLSLLYDRDSNIYKTDIPD 343
DB 301 IAGAPGAASFTVTLNLKANNT--QTAVNSCCVPTKRRLSLMLYFDNRNNVKTID 358
QY 344 MVEVACGCS 352
DB 359 MIVEACGCS 367

RESULT 2

QY 091XN3 PRELIMINARY; PRT; 350 AA.
AC Q91XN3;
DT 01-DEC-2001 (Tremblrel, 19, Created)
DT 01-DEC-2001 (Tremblrel, 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
DE INHIBIN BETA E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010404; AAI10404.1;
SO SEQUENCE 350 AA; 39002 MW; 9B7EA8AFAC389FA CRC64;

Query Match 31.88; Score 587.5; DB 11; Length 350;
Best Local Similarity 38.08; Pred. No. 1.8e-50;
Matches 141; Conservative 66; Mismatches 109; Indels 55; Gaps 14;

QY 5 L1LALFLPTTTPVVPKTEGPCPACWCAIFDLESORELLDLAKSLDKLHLSORPLIS 64
DB 12 L1MALVW-----QSTRSACPSGCGPTLAPQGRALVLELAKOILLEGHLTSRRIT 64
QY 65 PVSFGALKTALORLGR-----RETLLEHDOQEYEITISFAD--TDLSSINOTRLE 116
DB 65 RPLPQALTRLRRLQ--PKSWVPGNR-----KVISFATIIDKSTSTYRSMLT 111
QY 117 FHFSGRMAAGMEVOTRPFVOPPHNATOTMINIRVLRYPDNL-----TLTSQYVQVN 172
DB 112 FOLSLWLNH-----YNAIRLMLHVPSPFGLYLR--LFRGCTTRCGFRFLAEH--QT 163
QY 173 NASGWYOLLGHEAQAACSGHLEL-----VPSQVAHSSLLLGWFSHPPVAAQ 225
DB 164 TSSGHALLTLSSGLRSDSGVYKQLEFRPLDLNSTAAGLRPLLDPAQGOORPLEKI 223
QY 226 RVE--GKHVRARRGIDCGGRMCCROEFVDFREIGMNMIIOPEGYQINVCMLCPMH 283

DB 224 RANEPAGARRRRTPTCEBETPLCCCKRDHYVDFQELGMDWMLQDQGYLNCSSQCPRH 283
QY 284 VAGHGISASFTAVLNLKANA--AAGTTGSGCCVPTSRPLSLLYDRDSNIYKTDI 341
DB 284 LAGSPGIAASFHSAVPSLLKANPNPAGS-----SCCVPARBRLSLLYLDHNGNVYKTDV 339

QY 342 PDMVACGCS 352
DB 340 PDMVACGCS 350

RESULT 3

QY 091350 PRELIMINARY; PRT; 370 AA.
AC Q91350;
DT 01-NOV-1996 (Tremblrel, 01, Created)
DT 01-NOV-1996 (Tremblrel, 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
DE ACTIYIN BETA B SUBUNIT.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93273083; PubMed=8500654;
RA Dohrmann C.E., Hemmick-Brivanlou A., Thomson G.H., Fields A.,
RA Woolf T.M., Melton D.A.;
RT Expression of actiylin mRNA during early development in Xenopus
RT laevis.*;
RL dev. Biol. 157:474-483(1993).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DB EMBL; S61773; AAB26863.1;
DR HSSP; P18075; IBM.
DR InterPro; IPRO02400; GF_cysknot.
DR InterPro; IPRO01839; TGF-beta.
DR InterPro; IPRO01111; TGF-beta.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PRINTS; PR00436; GFCYSKNOT.
DR PRODOM; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
KW Glycoprotein.
SO SEQUENCE 370 AA; 41679 MW; AD21502ACA5F1DE9 CRC64;

Query Match 30.68; Score 566.5; DB 13; Length 370;
Best Local Similarity 34.78; Pred. No. 2.5e-48;
Matches 130; Conservative 73; Mismatches 137; Indels 35; Gaps 12;

QY 5 L1LALFLPTTTPVVPKTEGPCPACWCAIFDLESORELLDLAKSLDKLHLSORPLIS 62
DB 4 L1LPLLAGLARCADSPRPECCPSCHP--PMBP--MLEAVKHLITLMLHDDR 57
QY 63 LSPVSGALKTALORLGR-----TLLEHD-----QROEYEITISFADTDL 108
DB 58 ITMHWPAANVAVSLRKHLAAGVREDEGLLEIPDLDSGLSPRCHSTENSAELITFAETD 117
QY 109 SINOTRLEFHSGRMAAGMEVOTRPFVOPPH--NATOTMINIRVLRYPDNLTLT 165
DB 118 TASHVRLSTFIANGQNLNLFVQSNLMYLLKLEPVMDKSHRKIRIVVHODAFNPDKMN 177
QY 166 SQYVQVNASGWYOLLGHEAQAACSG--HLLELVPSQVAHSSLL-----GWFSSHP 219
DB 178 VEKVDVRRSGMHTFPLTAIQSLFEGERRLNLEVOCCGCEYVIAPIYVDPGESHP 237
QY 220 FVAAGVAV-EGKHVRARRGIDCGGRMCCROEFVDFREIGMNMIIOPEGYQINVCMLCPMH 278
DB 238 FLVYHAPLADNKKRIRKRGLECGHNTLCCROQFYIDFRILGNMDMIAPAGYGYVCG 297
QY 279 QCPHVAAGMGIASFTAVLNLKANA--AAGTTGSGCCVPTSRPLSLLYDRDSNIY 337

Db 298 SCRAVLAAGVGSASRHTAVNRYRMKGLNPGIV--NSCCIPKLSIMSLVFDDEINIV 355
 QY 338 KIDIPDMVNEACGCS 352
 Db 356 KRDPVPMIVDECGCA 370

RESULT 4

Q9PMG6 PRELIMINARY: PRT: 395 AA.
 ID Q9PMG6
 AC Q9PMG6
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ACTIVIN B.
 OS Anguilla japonica (Japanese eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
 OC Anguillidae; Anguilla.
 NCBI_Taxid=7937;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Mura T., Mura C., Eto Y., Nagehama Y.;
 RT "Activin B gene is required for the initiation of spermatogenesis in the Japanese eel, Anguilla japonica."
 CC Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
 DR -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL: AB025356; BAA83804.1; -
 DR HSSP: P12643; 38MP.
 DR InterPro: IPR000381; Inhibin_beta.
 DR InterPro: IPR001318; Inhibin_beta.
 DR InterPro: IPR001839; TGF-beta.
 DR pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGF_beta; 1.
 DR PRINTS: PR00671; INHIBINB.
 DR PRINTS: PR00672; INHIBINB.
 DR Prodom: PD000357; TGF-beta; 1.
 DR SMART: SM00204; TGF-beta; 1.
 DR PROSITE: PS00250; TGF_BETA; 1.
 KW Glycoprotein.
 SO SEQUENCE 395 AA: 43889 MW: FA56DD62D18509A3 CRC64;

Query Match 29.5%; Score 545.5; DB 13; Length 395;
 Best Local Similarity 32.2%; Pred. No. 3,5e-46;
 Matches 121; Conservative 78; Mismatches 136; Indels 41; Gaps 11;

QY 14 PPTVVAWPKTEGCPACWGAIFPLESORELL--LDLAKKSILDKLHLSORPILSRVSRCA 71
 Db 24 PGTETQTVSODTCASC--GLGQPEESGRMDIDFLVAVKRHLRLQMRPNTHPIPKXA 82
 QY 72 LKTAQRLR-GPRRE-----TLLEHDOREEYEISFADTDSINOTRLRPH 118
 Db 83 MYTALRLKLAGVREDGRIEIPNLDSHATYNNVEDTSEIISFAESD--ELTSSKSRH 140
 QY 119 F---SGRMAAGMEVROTREFEFVQFPHNATOTMIRVILRPY--DTNLTLS----- 166
 Db 141 FLISMEGNONLVLSQASLWLYFRLPLPSASEKSSRRKVTYVYQOTGAATAAAAAAGRW 200
 QY 167 ---QVAVQVNASGWYOLLGPEAOAASOGHLTLELVPSOVAHSSLIL-----GWPSH 217
 Db 201 GLVEKREVLKRSQWMTFLTEPRYKGVFERKDRRODLVRCCECAAAVLPVLVDPGDESH 260
 QY 218 RPFVAQVAV--EGKRVRRRGIDCOGSRMCCROEFVDFREIGNNDWIIOEGYAMNFC 276
 Db 261 RPFVLAQVRLADCKHRIKRGLECDOTGLCCROQYIDFLIGNNDWIILASGFGVNC 320
 QY 277 TQCCPLHVAAGMIGSASFTAVLNLKANAAGCTTGRGSCCVPTSRRLPILSLLYDRDSNI 336
 Db 321 EGCSPAVMAGVSSASFTAVVAVNRYRMKGLNPGIV--NSCCIPKLSIMSLVFDDEINIV 379

QY 337 VETDIPDMVNEACGCS 352
 Db 380 VKRDVPMIVDECGCA 395

RESULT 5

Q9HBP0 PRELIMINARY: PRT: 426 AA.
 ID Q9HBP0
 AC Q9HBP0
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 47.5 KDA PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
 RA Yu J., Han L.H.;
 RT "Novel Human cDNA clones with function of inhibiting cancer cell growth."
 CC Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 DR -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL: AF218018; AAG17260.1; -
 DR HSSP: P18075; 18MP.
 DR InterPro: IPR002405; Inhibin_alpha.
 DR InterPro: IPR000491; Inhibin_alpha.
 DR InterPro: IPR001318; Inhibin_beta.
 DR InterPro: IPR001839; TGF-beta.
 DR InterPro: IPR001111; TGF-beta.
 DR pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGF_beta; 1.
 DR PRINTS: PR00669; INHIBINA.
 DR PRINTS: PR00670; INHIBINA.
 DR PRINTS: PR00672; INHIBINB.
 DR Prodom: PD000357; TGF-beta; 1.
 DR SMART: SM00204; TGF-beta; 1.
 DR PROSITE: PS00250; TGF_BETA; 1.
 KW Glycoprotein; Hypothetical protein.
 SO SEQUENCE 426 AA: 47454 MW: 339276317BD5B408 CRC64;

Query Match 29.0%; Score 537; DB 4; Length 426;
 Best Local Similarity 31.2%; Pred. No. 2,7e-45;
 Matches 132; Conservative 69; Mismatches 140; Indels 82; Gaps 11;

QY 6 LLLLETPPTVWPKTEG-----PCPACWGAIF--DLESORELLDLAKKSILDKLHLS 58
 Db 10 LLASCMIIIVRSPPGSGHSAAPCPSCALALPKVDVNSQPEVAVKHLINMLHLK 69
 QY 59 ORPLSRPVSKALKTAQLR-----GPRRELLLEHDOREEYEIISF 102
 Db 70 KRDPVQVPPKALNALRLKLVGKGVNGVVEIEDIDGRAEM--NELMEQTSLETF 126
 QY 103 ADTDSISINOTRLRPHFEGSRMAAGMEVROTREFEFVQFPH--NATOT-MIRVILRPY-- 158
 Db 127 AE---SGARATLHREIEIKESGSDLSVERAEVMEFLKPKANRRTKVTTLTLPQOQHPO 183
 QY 159 -----DTNLTLSQVYVQVNASGWYOLLGPEAOAASOGHLTLEL-- 199
 Db 184 GSLDTGEAEAEVGLKGERSELLSEKVVDAKRSWHPVSSSIQRLLDQKSSLDVRIA 243
 QY 200 VPESOVAHSSLIL-----GWPSHPRFVAQVR--VEG 229
 Db 244 CEQCESASVLLGAKKKKKEBEDEGKKGEGGAGADEKESHRPFLMLQAROSEDH 303
 QY 230 KHRVRRRGIDCOGSRMCCROEFVDFREIGNNDWIIOEGYAMNFCCTGOCPLHVAAGMP 289
 Db 304 PHRRRRGLCEDGKVNICKCKKQFPVFRDIDGNDWIIILASGYHANYEBGDEPSHIACTSG 363
 QY 290 ISASFTAVLNLKANAAGCTTGRGSCCVPTSRRLPILSLLYDRDSNIVKTDIPDMVNEAC 349

RESULT 8

O9PWR8

PRELIMINARY: PRT: 392 AA.

AC O9PWR8: 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ACTIVIN BETA B SUBUNIT PRECURSOR.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Carassius.
 OX NCBI_Taxid=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RA MEDLINE-97424746; PubMed-9278859;
 RA Ge W., Miura T., Kobayashi H., Peter R.E., Nagahama Y.;
 RT "Cloning of cDNA for goldfish activin beta B subunit, and the
 RT expression of its mRNA in gonadal and non-gonadal tissues.";
 RL J. Mol. Endocrinol. 19:37-45(1997).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL: AF004659; AAB61468.1; -;
 DR HSSP: P12643; 3BMP.
 DR InterPro: IPR000381; Inhibin_beta.
 DR InterPro: IPR001318; Inhibin_beta.
 DR InterPro: IPR001839; TGF-beta.
 DR InterPro: IPR001111; TGF-beta.
 DR Pfam: PF00019; TGF-beta.1.
 DR Pfam: PF00688; TGF-beta-propeptide.1.
 DR PRINTS: PRO0671; INHIBINB.
 DR PRINTS: PRO0672; INHIBINB.
 DR ProDom: PD000357; TGF-beta.1.
 DR SMART: SM00204; TGF-beta.1.
 DR PROSITE: PS00250; TGF-BETA.1.
 DR GlycoProtein: Signal.
 FT SIGNAL 1 23
 FT CHAIN 277 392 ACTIVIN BETA B SUBUNIT.
 SO SEQUENCE 392 AA; 43853 MW; 73AAAT7E1C0B2450B CRC64;

Query Match 28.5%; Score 527; DB 13; Length 392;
 Best Local Similarity 33.1%; Pred. No. 2.5e-44;
 Matches 120; Conservative 75; Mismatches 129; Indels 38; Gaps 12;

23 EGCPCPC-MCAIFDLSQRELLDLAKKSLDOKLHLSORPILSRPSCRAKLTALORLNG 81
 DB ESOCACSCGLHPDDSGRMDTDFLEAVKRLHNLQMRERPNTHPTPKAAMVTALAKLHA 96
 OY 82 -----PREFTLLEHDQROEE-YELISFADTDLSSINQTRLEFHSGRMASGMEV 129
 DB 97 GKVEDGVEIPIFDGHAANEVEQETSELISFESDDVTPESSSLYFLISNGNONLYV 156
 OY 130 RQTR-FMEFVOPPHNATQTMNIRVLV-LRPYDTNLTLTQYV-----VOYNASGWQ 179
 DB 157 LQANLMLYFKLLPGTQEKGRKRVTVRVSYPEG---GQNVHMPMKERVELKRSQWHT 212
 OY 180 LLLGPEAOAASOGHLLTLEVPESQVAHSSLILGW-----SHRFVAAOV-RVEGKR 232
 DB 213 FYSEVSEVREKLAKGRRDDIHCECEANAVLPILVDSDFSHRFLVRAQAQASKIR 272
 OY 233 VRRGIDCOG-GSRMCCROEFVDFREIGWMDIIOPEGYAMNFCGQCPPLHVAWGPGIS 291
 DB 273 IRRGLECDCTNGCLCRODFYIDFLILGNMDIITAPAGYIGYCGSCPATMAGYPSGA 332
 OY 292 ASHTAVNLKLANA-AACTTGRGSCVPTSRRLSLLYYDRDSNIVKTDIDPMVEACG 350
 DB 333 SSHHTAVNVQYRMKGISPCSV--NSCIPTKLSTGMLYFDEYINIVKRDVPMIIVECG 390
 OY 351 CS 352
 DB 391 CA 392

RESULT 9

O98SP9

PRELIMINARY: PRT: 424 AA.

AC O98SP9: 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE INHIBIN-BETA.
 OS Meleagris gallinapavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 OX NCBI_Taxid=9103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RA Ahn J., You S., Kim H., Foster D.N., El Halawani M.E.;
 RT "Molecular cloning of turkey inhibin-alpha and beta subunits.";
 RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL: AF336338; AAK21265.1; -;
 DR HSSP: P18075; 1BMP.
 DR InterPro: IPR002405; Inhibin_alpha.
 DR InterPro: IPR000491; Inhibin_beta.
 DR InterPro: IPR001318; Inhibin_beta.
 DR InterPro: IPR001839; TGF-beta.
 DR InterPro: IPR001111; TGF-beta.
 DR Pfam: PF00019; TGF-beta.1.
 DR Pfam: PF00688; TGF-beta-propeptide.1.
 DR PRINTS: PRO0669; INHIBINA.
 DR PRINTS: PRO0670; INHIBINA.
 DR PRINTS: PRO0672; INHIBINB.
 DR ProDom: PD000357; TGF-beta.1.
 DR SMART: SM00204; TGF-beta.1.
 DR PROSITE: PS00250; TGF-BETA.1.
 DR GlycoProtein: Signal.
 SO SEQUENCE 424 AA; 47442 MW; B3E7CF3B9FDF0C59 CRC64;

Query Match 27.0%; Score 499; DB 13; Length 424;
 Best Local Similarity 30.4%; Pred. No. 1.8e-41;
 Matches 127; Conservative 65; Mismatches 152; Indels 74; Gaps 11;

6 LIALFLFPTTVVANKTEG-----PCPACWGAIF--DLSQRELLDLAKKSLDOKLHLS 58
 DB 10 LVIICMIYRSPPTGSESHSVTDCPSICALTTLSKDVPSQPEVAVKRLHNLMLHLR 69
 OY 59 QPILSRPVSRAKLTALORL-----GPRFTLLEHDQ-----QEEYEIISFADT 105
 DB 70 DRPNITQPVKAAALLNAILKHLVKGVDGQYVEIEDVGRINOMNEVEQETSEITTFQ 128
 OY 106 DLSINQTLFHFHS--GRMASGMEVROTRMFYQFPHNATQTMNIRVLVLRP----- 158
 DB 129 --SGTPKTLHFHEISKESELSVEHAEWLEFLKYSKANRSRTKTYTLFQOQROPKNS 186
 OY 159 -----DTNLTLTQYVVOVNAAGWYQLLGPDAOACSGHLLTLE---VPE 202
 DB 187 ESEDMEDGGLGERSSEILISEKAVDTKRSTWHITPVSSVORLLDQKSSLDVAIADL 246
 OY 203 SOVAHSSLT-----GWF-----SHRFVAAOV--VEGKR 234
 DB 247 COETGASLVLGKKKKKEDDEGKREKADAGELTGEERKQSHRFLMLLARISEDRQHR 306
 OY 235 RRGIDCOGSRMCCROEFVDFREIGWMDIIOPEGYAMNFCGQCPPLHVAWGPGISASF 294
 DB 307 KRGLECDGVNICKCKKQFSEKIDGMSDWIITAPYGHANVCEGCPSHIAGTSSSSLSF 366
 OY 295 HTAVNLKLANAAGTGTGSCVPTSRRLSLLYYDRDSNIVKTDIDPMVEACGCS 352
 DB 367 HSTVINHYRMGRHSPANLCKSCVPTKLRPMMLYTYDDGQNIKKIDQNIIVECGCS 424

RESULT 10

OY 286 GMPGISAFHTAVNLKANAAGTTGRCSCVPTSRRLPLSLYYDRDSNIVKTDIP 342
DB 64 GVPGSASSFHTAVNOYRMGRMS-PSGMNSCSCPTKTLSTMSMLYFDDEVNIYKRDVP 119

RESULT 13

OY 095N79 PRELIMINARY; PRT; 119 AA.
AC 095N79;
DT 01-DEC-2001 (TREMBLERL. 19, Created)
DT 01-DEC-2001 (TREMBLERL. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLERL. 19, Last annotation update)
DE ACTIVIN BETA-A (FRAGMENT).
OS Allutropoda melanoleuca (Giant panda).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Allutropoda.
OX NCBI_TaxID=9646;
RN 11
RP SEQUENCE FROM N.A.
RA Wang X., Wang Y., Wang X.;
RT "Cloning and Analysis of Activin Beta-A subunit in Giant Panda."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF502556; AAK38654.1;
FT NON_TER 1
FT SEQUENCE 119 AA; 13309 MW; 914DFB2F25D8218A CRC64;
SQ

Query Match 19.8%; Score 367; DB 6; Length 119;
Best Local Similarity 51.3%; Pred. No. 5.6e-29;
Matches 59; Conservative 20; Mismatches 36; Indels 0; Gaps 0;

OY 237 GICGCGSRMCCROEFFVDREIGNDWIIIOPEGYAMNFCGQCPPLHVAGMPCISAFHT 296
DB 3 GLECDGKVNICKCKKOFVSKDIGNDWIIAPSGYHANYCEGCEPHIAGTSGSSLSFHS 62
OY 297 AVNLKANAAGTTGRCSCVPTSRRLPLSLYYDRDSNIVKTDIPDMVVEACGC 351
DB 63 TVINHYMRGRHSPPANLKSVCPTKLRPMMLYDDGQNTIKKDIOMIVEECGC 117

RESULT 14

OY 095KP2 PRELIMINARY; PRT; 119 AA.
AC 095KP2;
DT 01-DEC-2001 (TREMBLERL. 19, Created)
DT 01-DEC-2001 (TREMBLERL. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLERL. 19, Last annotation update)
DE ACTIVIN SUBUNIT A (FRAGMENT).
OS Ursus malayanus (Malayan sun bear) (Helarctos malayanus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Helarctos.
OX NCBI_TaxID=9634;
RN 11
RP SEQUENCE FROM N.A.
RA Wang X., Wang Y., Wang X.;
RT "Molecular cloning of the activin gene A subunit mature peptide from RT Subunit related animals."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029554; AAK40341.1;
FT NON_TER 1
FT SEQUENCE 119 AA; 13309 MW; 914DFB2F25D8218A CRC64;
SQ

Query Match 19.8%; Score 367; DB 6; Length 119;
Best Local Similarity 51.3%; Pred. No. 5.6e-29;
Matches 59; Conservative 20; Mismatches 36; Indels 0; Gaps 0;

OY 237 GICGCGSRMCCROEFFVDREIGNDWIIIOPEGYAMNFCGQCPPLHVAGMPCISAFHT 296
DB 3 GLECDGKVNICKCKKOFVSKDIGNDWIIAPSGYHANYCEGCEPHIAGTSGSSLSFHS 62
OY 297 AVNLKANAAGTTGRCSCVPTSRRLPLSLYYDRDSNIVKTDIPDMVVEACGC 351

DB 63 TVINHYMRGRHSPPANLKSVCPTKLRPMMLYDDGQNTIKKDIOMIVEECGC 117

RESULT 15

OY 09W6T9 PRELIMINARY; PRT; 138 AA.
AC 09W6T9;
DT 01-NOV-1999 (TREMBLERL. 12, Created)
DT 01-NOV-1999 (TREMBLERL. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLERL. 19, Last annotation update)
DE ACTIVIN BETA B PROTEIN (FRAGMENT).
GN INHB OR ACTIVIN BETA B.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN 11
RP SEQUENCE FROM N.A.
RA MEDLINE-99307072; PubMed-10375499;
RA Rodaway A., Takeda H., Koshida S.,
RA Smith J.C., Patient R., Holder N.;
RT "Induction of the mesoderm in the zebrafish germ ring by yolk cell-derived TGF-(beta) family signals and discrimination of mesoderm and endoderm by FGF."
RL Development 126:3067-3077(1999).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AJ238981; CAB43092.1;
DR HSSP; P12643; 3BMP.
DR ZFIN; ZDB-GENE-990415-2; Inhb.
DR InterPro; IPR002400; GF_cyskn.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGF-beta.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
KW Glycoprotein.
FT NON_TER 1
FT SEQUENCE 138 AA; 15263 MW; 5BE38C763BDAC42B CRC64;
SQ

Query Match 19.3%; Score 357; DB 13; Length 138;
Best Local Similarity 50.8%; Pred. No. 6.9e-28;
Matches 61; Conservative 24; Mismatches 31; Indels 4; Gaps 3;

OY 234 RRRGIDCGGS-RMCCROEFFVDREIGNDWIIIOPEGYAMNFCGQCPPLHVAGMPCISA 292
DB 15 RGSFPCDGNNGCLCCROOFTYIDRLIGNDWIIAPAGYGCSCGPAYMAGPGSAS 74
OY 293 SFTAVNLKANA-AAGTTGRCSCVPTSRRLPLSLYYDRDSNIVKTDIPDMVVEACGC 351
DB 75 SFTAVNOYRMGRMSPGSV--NSCIPKLTSMMLYFDDEVNIYKRDVNMIVEECGC 132

Search completed: October 12, 2002, 02:08:42
Job time : 44 secs

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